

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 15:11:04 ; Search time 67 Seconds
(without alignments)
1915.053 Million cell updates/sec

Title: US-10-035-958-61

Perfect score: 223

Sequence: 1 MGWTNRLVTAAALLGLMMVV.....PTLQAPGRASEPKHKTRQR 223

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 6

Total number of hits satisfying chosen parameters: 6224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124	55.6	223	1	PBPL_HUMAN
2	11	4.9	242	1	PBPL_MOUSE
3	10	4.5	151	2	Q70JR7
4	10	4.5	151	2	CAE53888
5	10	4.5	173	2	Q75QX2
6	10	4.5	174	2	Q6R3R0
7	10	4.5	174	2	Q75QW8
8	10	4.5	174	2	Q76BW3
9	10	4.5	174	2	Q76BW4
10	10	4.5	174	2	Q76CA4
11	10	4.5	174	2	Q76CC3
12	10	4.5	174	2	Q76EQ5
13	10	4.5	174	2	BAD01561
14	10	4.5	174	2	BAD01576
15	10	4.5	174	2	BAD01612
16	10	4.5	174	2	AAS00056
17	10	4.5	174	2	BAD08337
18	10	4.5	174	2	BAD08338
19	10	4.5	174	2	BAD08340
20	10	4.5	174	2	BAD02371
21	10	4.5	174	2	BAD02372
22	10	4.5	176	2	Q7FTP7
23	10	4.5	177	2	Q84XL0
24	10	4.5	177	2	Q85XY9
25	10	4.5	178	2	Q8VWH2
26	10	4.5	179	2	Q93WI9
27	10	4.5	179	2	Q93WM7
28	10	4.5	202	2	Q9VI09
29	9	4.0	131	2	Q7PHU7
30	9	4.0	131	2	Q9BH16
31	9	4.0	185	2	Q6EUF9

32	9	4.0	2321	2	Q6RSR1	Q6r5r1 meleagrid h
33	9	4.0	2321	2	Q9DGT6	Q9dgt6 meleagrid h
34	9	4.0	2321	2	AAS01711	Aas01711 turkey he
35	9	4.0	2323	2	Q6HAA3	Q6haa3 meleagrid h
36	8	3.6	107	2	Q9FW01	Q9fw01 oryza sativ
37	8	3.6	121	2	Q88KR5	Q88kr5 pseudomonas
38	8	3.6	140	2	Q84XK8	Q84xk8 lycopersico
39	8	3.6	162	2	Q8LNF0	Q8lno oryza sativ
40	8	3.6	174	2	Q8LX54	Q8lxs4 cynocephalu
41	8	3.6	176	2	Q6XHR8	Q6xh8 drosophila
42	8	3.6	176	2	Q9VD01	Q9vd01 drosophila
43	8	3.6	176	2	AAR10138	Aar10138 drosophila
44	8	3.6	179	2	Q6J0U4	Q6j0u4 branchiosto
45	8	3.6	179	2	AAT38121	Aat38121 branchios
46	8	3.6	237	2	Q981S3	Q981s3 rhizobium l
47	8	3.6	313	2	Q73P79	Q73p79 treponema d
48	8	3.6	313	2	AAS11411	Aas11411 treponema
49	8	3.6	316	2	Q837T2	Q837t2 enterococcu
50	8	3.6	317	2	Q73Y94	Q73y94 mycobacteri
51	8	3.6	317	2	AAS04379	Aas04379 mycobacte
52	8	3.6	319	1	YD84_LISMO	Q8y7a4 listeria mo
53	8	3.6	319	2	Q71ZT6	Q71zt6 listeria mo
54	8	3.6	319	2	AAT04178	Aat04178 listeria
55	8	3.6	328	1	Y630_STRP3	Q8k7u2 streptococc
56	8	3.6	328	1	Y915_STRPY	Q9a064 streptococc
57	8	3.6	344	1	YF04_STRA3	Q9e498 streptococc
58	8	3.6	344	2	Q9WWY9	Q9wwy9 pseudomonas
59	8	3.6	383	2	Q88KB3	Q88kb3 pseudomonas
60	8	3.6	397	2	Q93J54	Q93j54 streptomyc
61	8	3.6	428	2	Q9L2D5	Q9l2d5 streptomyc
62	8	3.6	439	1	AKOA_HALN1	Q9hqc1 halobacteri
63	8	3.6	518	2	Q6NCL6	Q6nc16 rhodopsedu
64	8	3.6	518	2	CAE25900	CAe25900 rhodopsen
65	8	3.6	616	2	Q9H6K5	Q9hek5 homo sapien
66	8	3.6	821	2	Q9G74	Q8g74 bradyrhizob
67	8	3.6	1551	1	VGLM_DUGBV	Q02004 dugbe virus
68	7	3.1	26	2	Q9PS43	Q9ps43 gallus gall
69	7	3.1	26	2	Q9PS44	Q9ps44 gallus gall
70	7	3.1	27	2	Q9PRY4	Q9pry4 gallus gall
71	7	3.1	28	2	Q7LZ56	Q7lzs6 gallus gall
72	7	3.1	71	2	Q7QM25	Q7qm25 anopheles g
73	7	3.1	91	2	Q6I7M2	Q6i7m2 amblyomma t
74	7	3.1	93	2	Q8TM00	Q8tm00 methanosarc
75	7	3.1	93	2	Q7RH88	Q7rh88 plasmodium
76	7	3.1	100	2	Q6UG72	Q6ug72 sulfolobus
77	7	3.1	100	2	AAQ73268	AAq73268 sulfoblu
78	7	3.1	109	2	Q7B468	Q7b468 pseudomonas
79	7	3.1	109	2	Q9L176	Q9l176 pseudomonas
80	7	3.1	116	2	Q9TS16	Q9ts16 bos taurus
81	7	3.1	119	2	Q7UIU5	Q7uius rhodopirell
82	7	3.1	119	2	Q9KBF9	Q9kbf9 bacillus ha
83	7	3.1	126	2	Q8TWS3	Q8tws3 methanopyru
84	7	3.1	126	2	Q88RH7	Q88rh7 pseudomonas
85	7	3.1	134	1	D3_ONCVO	P54188 onchocerca
86	7	3.1	135	2	Q8T4K8	Q8t4k8 onchocerca
87	7	3.1	140	1	FLIL_BACSU	P23452 bacillus au
88	7	3.1	140	2	Q7W743	Q7w743 bordetella
89	7	3.1	148	2	Q6QXK9	Q6qxk9 agrotis seg
90	7	3.1	148	2	AAS82638	AAe82638 agrotis s
91	7	3.1	152	1	D1_ONCVO	P54186 onchocerca
92	7	3.1	152	2	Q7D0J5	Q7d0j5 agrobacteri
93	7	3.1	152	2	Q8UH39	Q8uh39 agrobacteri
94	7	3.1	172	2	Q6FIE3	Q6fie3 homo sapien
95	7	3.1	172	2	Q8BNB8	Q8bnb8 homo sapien
96	7	3.1	172	2	Q9H0W4	Q9h0w4 homo sapien
97	7	3.1	172	2	Q96AW1	Q96aw1 homo sapien
98	7	3.1	172	2	Q8C0B7	Q8c0b7 mus musculu
99	7	3.1	172	2	Q8RIC3	Q8ric3 mus musculu
100	7	3.1	174	2	Q7XUF1	Q7xuf1 oryza sativ
101	7	3.1	175	1	FT_ARATH	Q9exz2 arabidopsis
102	7	3.1	175	1	TSF_ARATH	Q9s7r5 arabidopsis
103	7	3.1	175	2	Q84XK9	Q84xk9 lycopersico
104	7	3.1	175	2	AAL38819	Aal38819 arabidops

105	7	3.1	175	2	AAM91747	Aam91747 arabidops	178	7	3.1	250	2	Q84BE9	Q84be9 uncultured
106	7	3.1	176	2	Q7OBM5	Q7obm5 legionella	179	7	3.1	250	2	Q84C12	Q84c12 uncultured
107	7	3.1	176	2	CAE53081	Caes53081 legionell	180	7	3.1	250	2	Q84C22	Q84c22 uncultured
108	7	3.1	179	2	Q9VD02	Q9vd02 drosophila	181	7	3.1	250	2	Q84C23	Q84c23 uncultured
109	7	3.1	184	2	Q9XHW5	Q9xhw5 oryza sativ	182	7	3.1	250	2	Q84C24	Q84c24 uncultured
110	7	3.1	186	1	PEBP_BOVIN	P13696 bos taurus	183	7	3.1	250	2	Q84C25	Q84c25 uncultured
111	7	3.1	186	1	PEBP_HUMAN	P30086 homo sapien	184	7	3.1	250	2	Q84C27	Q84c27 uncultured
112	7	3.1	186	1	PEBP_MACFA	P48737 macaca fasc	185	7	3.1	250	2	Q84C28	Q84c28 uncultured
113	7	3.1	186	1	PEBP_MOUSE	P70296 mus musculu	186	7	3.1	250	2	Q84C29	Q84c29 uncultured
114	7	3.1	186	1	PEBP_RAT	P31044 rattus norv	187	7	3.1	250	2	AAT12291	Aat12291 unculture
115	7	3.1	186	2	Q61RMO	Q61rm0 xenopus lae	188	7	3.1	251	2	Q6J5K4	Q6j5k4 uncultured
116	7	3.1	186	2	Q6GPR7	Q6gpr7 xenopus lae	189	7	3.1	251	2	Q6PL04	Q6pl04 uncultured
117	7	3.1	186	2	AAH70868	Aah70868 xenopus l	190	7	3.1	251	2	Q6PL05	Q6pl05 uncultured
118	7	3.1	187	1	PEB2_MOUSE	Q8vin1 mus musculu	191	7	3.1	251	2	Q83US4	Q83us4 uncultured
119	7	3.1	187	2	Q8VI08	Q8vi08 drosophila	192	7	3.1	251	2	Q84C11	Q84c11 uncultured
120	7	3.1	187	2	Q8WK67	Q8wk67 oryctolagus	193	7	3.1	251	2	Q84C14	Q84c14 uncultured
121	7	3.1	187	2	Q6NYS4	Q6nys4 brachydanio	194	7	3.1	251	2	Q84C15	Q84c15 uncultured
122	7	3.1	187	2	Q7ZUV8	Q7zuv8 brachydanio	195	7	3.1	251	2	Q84C16	Q84c16 uncultured
123	7	3.1	187	2	AAH63171	Aah63171 rattus no	196	7	3.1	251	2	Q99QB3	Q99qb3 uncultured
124	7	3.1	187	2	AAH66479	Aah66479 brachydan	197	7	3.1	251	2	Q9AFB5	Q9afe5 uncultured
125	7	3.1	190	2	O54564	O54564 halobacteri	198	7	3.1	251	2	Q9AFB6	Q9afe6 uncultured
126	7	3.1	190	2	O7PYP6	O7pyp6 anopheles g	199	7	3.1	251	2	Q9AFB7	Q9afe7 uncultured
127	7	3.1	194	2	Q6CFV4	Q6cfv4 yarrowia li	200	7	3.1	251	2	Q9AFB8	Q9afe8 uncultured
128	7	3.1	194	2	Q6MD84	Q6md84 parachlamyd	201	7	3.1	251	2	Q9AFB9	Q9afe9 uncultured
129	7	3.1	194	2	P73381	P73381 synechocyst	202	7	3.1	251	2	Q9AFF1	Q9aff1 uncultured
130	7	3.1	194	2	CAF23465	Ca23465 parachlam	203	7	3.1	251	2	Q9AFF3	Q9aff3 uncultured
131	7	3.1	195	2	Q6FTN2	Q6ftn2 oryza sativ	204	7	3.1	251	2	Q9AFF4	Q9aff4 uncultured
132	7	3.1	195	2	Q9RWJ5	Q9rwj5 deinococcus	205	7	3.1	251	2	Q9AFF5	Q9aff5 uncultured
133	7	3.1	197	1	OVI16_ONCVO	P31729 onchocerca	206	7	3.1	251	2	AAT09902	Aat09902 unculture
134	7	3.1	201	1	YL79_YEAST	Q06252 saccharomyc	207	7	3.1	251	2	AAT09903	Aat09903 unculture
135	7	3.1	204	2	Q751Y1	Q751y1 ashbya goss	208	7	3.1	251	2	AAT09900	Aat09900 unculture
136	7	3.1	204	2	AAS54066	Aas54066 ashbya go	209	7	3.1	252	2	Q9AFG0	Q9afg0 uncultured
137	7	3.1	210	2	Q6FX79	Q6fx79 candida gla	210	7	3.1	252	2	Q9AFG0	Q9afg0 uncultured
138	7	3.1	211	2	Q85PT6	Q85pt6 anopheles g	211	7	3.1	252	2	O6LJ99	O6lj99 photobacter
139	7	3.1	214	2	Q7PWN1	Q7pwn1 anopheles g	212	7	3.1	252	2	CAG22631	Ca22631 photobact
140	7	3.1	216	2	Q9F3F7	Q9f3f7 streptomyce	213	7	3.1	255	2	Q7MDW6	Q7mdw6 vibrio vuln
141	7	3.1	220	2	Q8LIH4	Q8lih4 oryza sativ	214	7	3.1	255	2	Q8D705	Q8d705 vibrio vuln
142	7	3.1	221	1	PBPB_CAEEL	O16264 caenorhabdi	215	7	3.1	257	2	Q9VK60	Q9vk60 drosophila
143	7	3.1	222	2	Q9YDN2	Q9ydn2 aeropyrum p	216	7	3.1	257	2	Q84C20	Q84c20 uncultured
144	7	3.1	224	2	Q7OHM0	Q7ohw0 anopheles g	217	7	3.1	258	2	Q84C21	Q84c21 uncultured
145	7	3.1	225	2	Q8YD7	Q8y7d7 anabaena sp	218	7	3.1	260	2	Q72GY4	Q72gy4 thermus the
146	7	3.1	233	2	Q6FRC1	Q6frc1 candida gla	219	7	3.1	260	2	AAS82054	Aas82054 thermus t
147	7	3.1	234	2	Q9UIR1	Q9uir1 caenorhabdi	220	7	3.1	264	2	Q6U683	Q6u683 plethodon p
148	7	3.1	239	2	Q94J24	Q94j24 oryza sativ	221	7	3.1	264	2	Q6U684	Q6u684 plethodon w
149	7	3.1	240	2	Q7MVU6	Q7mvu6 porphyromon	222	7	3.1	264	2	AAR23481	Aar23481 plethodon
150	7	3.1	241	2	Q7PVP5	Q7pvp5 anopheles g	223	7	3.1	264	2	AAR23482	Aar23482 plethodon
151	7	3.1	241	2	Q7QHV9	Q7qhv9 anopheles g	224	7	3.1	266	2	Q9RWF5	Q9rwf5 deinococcus
152	7	3.1	243	2	Q84CY2	Q84cy2 uncultured	225	7	3.1	267	2	Q7S9X5	Q7s9x5 neurospora
153	7	3.1	244	2	Q9P6X9	Q9p6x9 neurospora	226	7	3.1	269	2	Q9FAH1	Q9fah1 pseudomonas
154	7	3.1	247	2	Q84C13	Q84c13 uncultured	227	7	3.1	270	2	Q9FAH2	Q9fah2 pseudomonas
155	7	3.1	249	1	PRRG_PRR01	Q9f7p4 gamma-prote	228	7	3.1	276	2	Q8ENK6	Q8enk6 oceanobacil
156	7	3.1	249	2	Q84C31	Q84c31 uncultured	229	7	3.1	284	2	Q73L36	Q73l36 treponema d
157	7	3.1	249	2	Q84C32	Q84c32 uncultured	230	7	3.1	284	2	AAS12543	Aas12543 treponema
158	7	3.1	249	2	Q9AFF0	Q9aff0 uncultured	231	7	3.1	286	1	CYSW_SYN7	Cysw_syn7 mycobacteri
159	7	3.1	249	2	Q9AFF2	Q9aff2 uncultured	232	7	3.1	286	2	Q9CCW1	Q9ccw1 mycobacteri
160	7	3.1	249	2	AAO73908	Aao73908 unculture	233	7	3.1	287	2	Q6GL77	Q6gl77 xenopus tro
161	7	3.1	249	2	AAT09901	Aat09901 unculture	234	7	3.1	291	2	Q7WYG8	Q7wyg8 pseudomonas
162	7	3.1	250	2	Q674G7	Q6j4g7 uncultured	235	7	3.1	292	1	LICB_HAEIN	Licb_haeinophilus
163	7	3.1	250	2	Q83TG9	Q83tg9 uncultured	236	7	3.1	293	2	Q9L396	Q9l396 shingomona
164	7	3.1	250	2	Q83TU0	Q83tu0 uncultured	237	7	3.1	297	1	U33K_HUMAN	U04323 homo sapien
165	7	3.1	250	2	Q83UH6	Q83uh6 uncultured	238	7	3.1	305	1	Y348_MYCPN	Y75255 mycoplasma
166	7	3.1	250	2	Q84BD7	Q84bd7 uncultured	239	7	3.1	312	2	Q8BV93	Q8bv93 homo sapien
167	7	3.1	250	2	Q84BD8	Q84bd8 uncultured	240	7	3.1	313	2	Q8DS49	Q8ds49 streptococc
168	7	3.1	250	2	Q84BD9	Q84bd9 uncultured	241	7	3.1	313	2	Q93HA6	Q93ha6 streptomyce
169	7	3.1	250	2	Q84BE0	Q84be0 uncultured	242	7	3.1	315	1	HEM3_PROMA	Hem3_proma prochloroc
170	7	3.1	250	2	Q84BE1	Q84be1 uncultured	243	7	3.1	318	2	Q8KN69	Q8kn69 pseudomonas
171	7	3.1	250	2	Q84BE2	Q84be2 uncultured	244	7	3.1	318	2	Q8KN93	Q8kn93 pseudomonas
172	7	3.1	250	2	Q84BE3	Q84be3 uncultured	245	7	3.1	319	1	YE21_LJISN	Y92bx1 listeria in
173	7	3.1	250	2	Q84BE4	Q84be4 uncultured	246	7	3.1	325	2	Q982B7	Q982b7 rhizobium l
174	7	3.1	250	2	Q84BE5	Q84be5 uncultured	247	7	3.1	334	2	Q72HV3	Q72hv3 thermus the
175	7	3.1	250	2	Q84BE6	Q84be6 uncultured	248	7	3.1	334	2	AAS81721	Aas81721 thermus t
176	7	3.1	250	2	Q84BE7	Q84be7 uncultured	249	7	3.1	335	2	Q8CGG5	Q8cgg5 mus musculu
177	7	3.1	250	2	Q84BE8	Q84be8 uncultured	250	7	3.1	335	2	AAH58570	Aah58570 mus muscu

251	7	3.1	339	2	Q87DU2	Q87du2 xylella fas	324	7	3.1	494	1	MURE_ECOLI	P22188 escherichia
252	7	3.1	340	2	Q8OXU5	Q80xu5 mus musculus	325	7	3.1	494	2	Q82M13	Q82m13 streptomyce
253	7	3.1	347	2	Q25436	Q25436 mayetiola d	326	7	3.1	495	1	MURE_SHIFL	Q83mg0 shigella fl
254	7	3.1	349	2	Q72HL7	Q72hl7 thermus the	327	7	3.1	496	2	Q23767	Q23767 culex tarsa
255	7	3.1	349	2	AAS81812	Aas81812 thermus t	328	7	3.1	497	2	Q6MW17	Q6mw17 neurospora
256	7	3.1	359	2	Q8TXS2	Q8txs2 mechanopyru	329	7	3.1	497	2	CAE76134	CaE76134 neurospora
257	7	3.1	361	1	Y136_METJA	Q57600 methanococ	330	7	3.1	502	2	Q74002	Q74002 pyrococcus
258	7	3.1	363	2	Q8CCB5	Q8ccb5 mus musculus	331	7	3.1	503	2	Q7WC94	Q7wc94 bordetella
259	7	3.1	364	1	WNT6_MOUSE	P22727 mus musculus	332	7	3.1	503	2	Q8AYE4	Q8aye4 brachydanio
260	7	3.1	364	2	Q8OZM9	Q80zm9 mus musculus	333	7	3.1	504	2	Q9ZBW5	Q9zbw5 streptomyce
261	7	3.1	365	1	WNT6_HUMAN	Q9y6f9 homo sapien	334	7	3.1	506	2	Q7P213	Q7p213 chromobacte
262	7	3.1	365	2	AAP36124	Aap36124 homo sapi	335	7	3.1	509	2	Q7WQ98	Q7wq98 bordetella
263	7	3.1	368	1	UCR2_TFAST	P07257 saccharomyc	336	7	3.1	509	2	Q9AK17	Q9ak17 streptomyce
264	7	3.1	368	2	AAS56394	Aas56394 saccharom	337	7	3.1	523	2	Q9KYG3	Q9kyg3 streptomyce
265	7	3.1	375	1	OTC_TRAHI	P78603 trametes hi	338	7	3.1	527	2	Q7XDX5	Q7xdx5 oryza sativ
266	7	3.1	375	2	Q8DYP2	Q8dyp2 streptococ	339	7	3.1	529	2	Q8N2D6	Q8n2d6 homo sapien
267	7	3.1	375	2	Q8B499	Q8e499 streptococ	340	7	3.1	529	2	Q726G5	Q726g5 desulfovibr
268	7	3.1	376	2	Q8GBA1	Q8gbal heliobacill	341	7	3.1	529	2	Q910E1	Q910e1 pseudomonas
269	7	3.1	377	2	Q6XZY1	Q6xzy1 pasteurella	342	7	3.1	529	2	Q910E1	Q910e1 pseudomonas
270	7	3.1	377	2	AAP80228	Aap80228 pasteurel	343	7	3.1	530	2	AAS97613	Aas97613 desulfovi
271	7	3.1	382	2	Q7U5K7	Q7u5k7 synecococ	344	7	3.1	531	2	Q838Q4	Q838q4 enterococu
272	7	3.1	382	2	Q6X2X6	Q6x2x6 pasteurella	345	7	3.1	531	2	Q74B43	Q74b43 geobacter s
273	7	3.1	382	2	AAP80233	Aap80233 pasteurel	346	7	3.1	531	2	Q6PA74	Q6pa74 xenopus lae
274	7	3.1	384	2	Q61340	Q61340 mus musculus	347	7	3.1	531	2	AAR35575	Aar35575 geobacter
275	7	3.1	387	2	Q99X15	Q99x15 staphylococ	348	7	3.1	531	2	AAH60427	Aah60427 xenopus l
276	7	3.1	387	2	Q7A7Z0	Q7a7z0 staphylococ	349	7	3.1	539	2	Q72KI2	Q72ki2 thermus the
277	7	3.1	388	2	Q966V2	Q966v2 halocynthia	350	7	3.1	539	2	AAS80826	Aas80826 thermus t
278	7	3.1	389	2	Q56074	Q56074 streptomyce	351	7	3.1	563	2	Q7NV85	Q7nv85 chromobacte
279	7	3.1	389	2	Q7WTF9	Q7wtf9 streptomyce	352	7	3.1	565	2	Q7QT28	Q7qt28 giardia lam
280	7	3.1	399	2	Q88GZ9	Q88gz9 pseudomonas	353	7	3.1	577	2	Q7RSE4	Q7rse4 plasmodium
281	7	3.1	408	2	Q916L7	Q916l7 pseudomonas	354	7	3.1	582	2	Q8PIQ4	Q8piq4 streptococ
282	7	3.1	404	2	Q7NXX06	Q7nx06 chromobacte	355	7	3.1	584	2	Q8K778	Q8k778 streptococ
283	7	3.1	411	2	Q73P30	Q73p30 treponema d	356	7	3.1	588	2	Q74GI5	Q74gi5 geobacter s
284	7	3.1	411	2	AAS11460	Aas11460 treponema	357	7	3.1	588	2	AAR33595	Aar33595 geobacter
285	7	3.1	412	2	Q8VBX7	Q8vbx7 mus musculus	358	7	3.1	602	2	Q87UA7	Q87ua7 pseudomonas
286	7	3.1	412	2	Q8VEI3	Q8vei3 mus musculus	359	7	3.1	604	2	Q8EMC2	Q8emc2 mycoplasma
287	7	3.1	412	2	Q8VI77	Q8vi77 mus musculus	360	7	3.1	605	2	Q8PB84	Q8pb84 xanthomonas
288	7	3.1	420	2	Q9A5Y2	Q9a5y2 caulobacter	361	7	3.1	612	2	P92916	P92916 allium cepa
289	7	3.1	420	2	Q9X8Q9	Q9x8q9 streptomyce	362	7	3.1	615	2	Q93H48	Q93h48 streptomyce
290	7	3.1	424	2	Q74EL2	Q74el2 geobacter s	363	7	3.1	619	2	Q6BIU3	Q6biu3 debaryomyce
291	7	3.1	424	2	AAR34277	Aar34277 geobacter	364	7	3.1	619	2	Q7TT41	Q7tt41 mus musculus
292	7	3.1	425	2	Q73PS3	Q73ps3 treponema d	365	7	3.1	619	2	Q91XT2	Q91xt2 mus musculus
293	7	3.1	425	2	AAS11216	Aas11216 treponema	366	7	3.1	621	2	Q6L970	Q6l970 anguilla ja
294	7	3.1	426	2	Q7S7G7	Q7s7g7 neurospora	367	7	3.1	621	1	LAC2_PODAN	P78722 podospora a
295	7	3.1	428	2	Q7W6W3	Q7w6w3 bordetella	368	7	3.1	622	2	Q8U9J0	Q8u9j0 agrobacteri
296	7	3.1	428	2	Q7WIZ6	Q7wiz6 bordetella	369	7	3.1	625	2	Q89FI4	Q89fi4 bradyrhizob
297	7	3.1	434	2	Q82D24	Q82d24 yersinia pe	370	7	3.1	628	2	Q6HLD7	Q6hld7 bacillus th
298	7	3.1	437	2	Q9JRV5	Q9jrv5 neisseria m	371	7	3.1	628	2	Q73B82	Q73b82 bacillus ce
299	7	3.1	437	2	Q9JUF6	Q9juf6 neisseria m	372	7	3.1	628	2	Q81TS3	Q81ts3 bacillus an
300	7	3.1	438	1	FUNC_SULSO	P39461 sulfolobus	373	7	3.1	628	2	Q9A4M9	Q9a4m9 caulobacter
301	7	3.1	439	2	Q96Z05	Q96z05 sulfolobus	374	7	3.1	628	2	AAS40467	Aas40467 bacillus
302	7	3.1	447	2	Q9HPQ2	Q9hpq2 halobacteri	375	7	3.1	629	1	FBW7_MOUSE	Q8ybv4 mus musculus
303	7	3.1	451	2	Q895M4	Q895m4 clostridium	376	7	3.1	639	2	Q07639	Q07639 streptomyce
304	7	3.1	453	2	Q58973	Q58973 pyrococcus	377	7	3.1	642	2	Q7CT69	Q7ct69 agrobacteri
305	7	3.1	460	2	Q8DOU0	Q8dou0 yersinia pe	378	7	3.1	643	2	Q7R868	Q7r868 plasmodium
306	7	3.1	460	2	AAS62600	Aas62600 yersinia	379	7	3.1	653	2	Q6CUH7	Q6cu7 kluyveromyc
307	7	3.1	461	2	Q9RSC9	Q9rsc9 deinococcus	380	7	3.1	659	1	VATI_PYRAB	Q6uxu2 pyrococcus
308	7	3.1	462	2	Q97XM0	Q97xm0 sulfolobus	381	7	3.1	662	2	Q6N8D8	Q6n8d8 rhodospseud
309	7	3.1	463	2	Q8RZN2	Q8rzn2 oryza sativ	382	7	3.1	662	2	CAE27406	CaE27406 rhodospes
310	7	3.1	464	1	NORM_HAEIN	P45272 haemophilus	383	7	3.1	690	2	Q892U7	Q892u7 clostridium
311	7	3.1	466	2	Q7SH39	Q7sh39 neurospora	384	7	3.1	704	1	DF3E_RHOCA	Q68045 rhodobacter
312	7	3.1	466	2	CAE76521	CaE76521 neurospor	385	7	3.1	707	1	FBW7_HUMAN	Q69690 homo sapien
313	7	3.1	467	2	Q7SZQ0	Q7szq0 brachydanio	386	7	3.1	723	2	Q8PJV9	Q8pjv9 xanthomonas
314	7	3.1	470	2	Q6NGG0	Q6ngg0 corynebacte	387	7	3.1	729	2	Q8AVI6	Q8avi6 xenopus lae
315	7	3.1	470	2	CAE50087	CaE50087 corynebac	388	7	3.1	744	2	Q7S073	Q7s073 neurospora
316	7	3.1	472	2	Q808Z8	Q808z8 rubella vir	389	7	3.1	766	2	Q9HWZ1	Q9hwz1 pseudomonas
317	7	3.1	477	2	Q8VH25	Q8vhn25 cavia porc	390	7	3.1	827	2	Q7LYC3	Q7lyc3 listeria mo
318	7	3.1	482	2	Q6V7R1	Q6v7r1 burkholderi	391	7	3.1	832	2	AAT04691	Aat04691 listeria
319	7	3.1	482	2	AAQ54965	Aaq54965 burkholder	392	7	3.1	832	2	Q98GU5	Q98gu5 rhizobium l
320	7	3.1	484	2	Q9RZ17	Q9rz17 deinococcus	393	7	3.1	853	2	Q7S3C5	Q7s3c5 neurospora
321	7	3.1	493	1	Q9W6M0	Q9w6m0 oreochromis	394	7	3.1	875	2	Q6BS08	Q6bs08 debaryomyce
322	7	3.1	494	1	MURE_ECOL57	Q8x922 escherichia	395	7	3.1	890	2	Q53582	Q53582 streptomyce
323	7	3.1	494	1	MURE_ECOL6	Q8f167 escherichia	396	7	3.1	893	2	Q7RIT3	Q7rit3 plasmodium

397	7	3.1	923	2	Q6YU66	Q6YU66 oryza sativ	470	6	2.7	58	2	Q9DIQ2	Q9DIQ2 hepatitis c
398	7	3.1	923	2	BAD1710	BAD1710 oryza sat	471	6	2.7	58	2	Q9DIQ9	Q9DIQ9 hepatitis c
399	7	3.1	992	2	Q9NTH6	Q9NTH6 homo sapien	472	6	2.7	58	2	Q9DIR1	Q9DIR1 hepatitis c
400	7	3.1	1042	2	Q9LMO1	Q9LMO1 zea mays (m	473	6	2.7	59	2	Q97R86	Q97R86 streptococc
401	7	3.1	1052	2	Q88532	Q88532 mus musculus	474	6	2.7	61	1	Y108_RICCN	Y108_RICCN rickettsia
402	7	3.1	1054	2	Q6GPM1	Q6GPM1 xenopus lae	475	6	2.7	62	2	Q9ADK3	Q9ADK3 escherichia
403	7	3.1	1057	2	Q9GKR1	Q9GKR1 homo sapien	476	6	2.7	62	2	Q9AB12	Q9AB12 caulobacter
404	7	3.1	1070	2	Q84M87	Q84M87 oryza sativ	477	6	2.7	63	2	Q84UK3	Q84UK3 lactobacill
405	7	3.1	1083	2	Q7Q7E2	Q7Q7E2 anopheles g	478	6	2.7	64	2	Q8JPP5	Q8JPP5 hepatitis c
406	7	3.1	1103	2	Q92MY6	Q92MY6 rhizobium m	479	6	2.7	64	2	Q8JPP6	Q8JPP6 hepatitis c
407	7	3.1	1111	2	Q87XD3	Q87XD3 pseudomonas	480	6	2.7	64	2	Q8JPP7	Q8JPP7 hepatitis c
408	7	3.1	1196	2	Q6FTP3	Q6FTP3 candida gla	481	6	2.7	64	2	Q8JPP9	Q8JPP9 hepatitis c
409	7	3.1	1225	2	Q6GP61	Q6GP61 xenopus lae	482	6	2.7	64	2	Q73XU4	Q73XU4 mycobacteri
410	7	3.1	1239	2	Q9FBR4	Q9FBR4 streptomyc	483	6	2.7	67	2	Q7VL71	Q7VL71 haemophilus
411	7	3.1	1345	2	Q6BIF0	Q6BIF0 debaromyce	484	6	2.7	67	2	AAS04531	AAS04531 mycobacte
412	7	3.1	1382	2	Q6IFU0	Q6IFU0 schistosoma	485	6	2.7	68	2	Q7SSK9	Q7SSK9 neurospora
413	7	3.1	1434	2	Q7XSJ4	Q7XSJ4 oryza sativ	486	6	2.7	68	2	Q05625	Q05625 staphylococ
414	7	3.1	1456	2	Q9UPV0	Q9UPV0 homo sapien	487	6	2.7	68	2	Q8JPF8	Q8JPF8 hepatitis c
415	7	3.1	1460	2	Q8LMT8	Q8LMT8 oryza sativ	488	6	2.7	68	2	Q8JPG0	Q8JPG0 hepatitis c
416	7	3.1	1516	1	NC02_XENLA	Q9W705 xenopus lae	489	6	2.7	71	1	TRAD_AGR5	Q44347 agrobacteri
417	7	3.1	1517	2	Q7UWF1	Q7UWF1 rhodospirell	490	6	2.7	71	1	TRAD_AGR5	Q44347 agrobacteri
418	7	3.1	1587	1	LMG3_HUMAN	Q9Y6N6 homo sapien	491	6	2.7	71	2	Q8TET5	Q8TET5 homo sapien
419	7	3.1	1646	2	Q88D40	Q88D40 pseudomonas	492	6	2.7	71	2	Q20922	Q20922 metallura t
420	7	3.1	1694	2	Q6MZL5	Q6MZL5 homo sapien	493	6	2.7	72	2	Q20915	Q20915 metallura b
421	7	3.1	1694	2	CAB46015	CAB46015 homo sapi	494	6	2.7	72	2	Q20925	Q20925 chalcostigm
422	7	3.1	1881	2	Q9L7Q2	Q9L7Q2 streptococc	495	6	2.7	72	2	Q20927	Q20927 eriocnemis
423	7	3.1	1876	2	Q8D4R5	Q8D4R5 vibrio vuln	496	6	2.7	72	2	Q6P3A5	Q6P3A5 mus muscu
424	7	3.1	1879	1	TRIA_HUMAN	Q15643 homo sapien	497	6	2.7	72	2	AAB64104	AAB64104 mus muscu
425	7	3.1	2160	2	Q13328	Q13328 magnaporthe	498	6	2.7	72	2	Q20913	Q20913 metallura w
426	7	3.1	2160	2	Q13488	Q13488 magnaporthe	499	6	2.7	73	2	Q20914	Q20914 metallura w
427	7	3.1	2310	2	Q7PQ11	Q7PQ11 anopheles g	500	6	2.7	73	2	Q20916	Q20916 metallura p
428	7	3.1	3054	2	Q7RXY5	Q7RXY5 neurospora	501	6	2.7	73	2	Q20917	Q20917 metallura o
429	7	3.1	3298	2	Q9VB11	Q9VB11 drosophila	502	6	2.7	73	2	Q20918	Q20918 metallura t
430	7	3.1	3853	2	Q8IJW2	Q8IJW2 plasmodium	503	6	2.7	73	2	Q20919	Q20919 metallura e
431	7	3.1	3953	2	Q6H253	Q6H253 burkholderi	504	6	2.7	73	2	Q20920	Q20920 metallura a
432	7	3.1	4067	2	Q6Z2J4	Q6Z2J4 actinoplan	505	6	2.7	73	2	Q20923	Q20923 metallura t
433	7	3.1	4067	2	Q70AZ7	Q70AZ7 actinoplan	506	6	2.7	73	2	Q20924	Q20924 chalcostigm
434	7	3.1	4067	2	CAE53352	CAE53352 actinopla	507	6	2.7	73	2	Q21805	Q21805 metallura t
435	7	3.1	4067	2	CAG15011	CAG15011 actinopla	508	6	2.7	73	2	Q21805	Q21805 metallura t
436	7	3.1	4077	2	Q939Z0	Q939Z0 amycolatops	509	6	2.7	73	2	Q88RU7	Q88RU7 pseudomonas
437	7	3.1	6084	2	Q87ID8	Q87ID8 vibrio para	510	6	2.7	73	2	Q92L43	Q92L43 helicobacte
438	7	3.1	7158	2	Q23551	Q23551 caenothabdi	511	6	2.7	74	2	Q25482	Q25482 helicobacte
439	6	2.7	15	2	Q71A41	Q71A41 homo sapien	512	6	2.7	74	2	Q3DW87	Q3DW87 rat cytomeg
440	6	2.7	15	2	AAQ11189	AAQ11189 homo sapi	513	6	2.7	75	2	Q7V603	Q7V603 prochloroco
441	6	2.7	19	2	Q47049	Q47049 enterobacte	514	6	2.7	77	2	Q47772	Q47772 enterococcu
442	6	2.7	20	1	CPBX_CAVPO	P34033 cavia porce	515	6	2.7	78	2	Q85FN9	Q85FN9 adiantum ca
443	6	2.7	21	2	Q9TWJ2	Q9TWJ2 symbiodiniu	516	6	2.7	78	2	Q89DK7	Q89DK7 bradyrhizob
444	6	2.7	31	2	Q9QVA5	Q9QVA5 cavia (guin	517	6	2.7	79	2	Q6L2P9	Q6L2P9 methanococc
445	6	2.7	33	2	Q9QVJ4	Q9QVJ4 cavia (guin	518	6	2.7	79	2	Q7XV02	Q7XV02 oryza sativ
446	6	2.7	35	2	Q80XC1	Q80XC1 mus musculu	519	6	2.7	79	2	CAF30131	CAF30131 methanoco
447	6	2.7	37	1	RL36_VIBCH	P78001 vibrio chol	520	6	2.7	80	1	OAG1_SALTI	OAG1_SALTI salmonella
448	6	2.7	38	1	RL36_BUCBP	Q89A86 buchnera ap	521	6	2.7	80	2	Q77WZ5	Q77WZ5 hepatitis c
449	6	2.7	40	2	Q9VZP8	Q9VZP8 hepatitis c	522	6	2.7	80	2	Q77WZ6	Q77WZ6 hepatitis c
450	6	2.7	41	2	Q9QYU1	Q9QYU1 cavia (guin	523	6	2.7	80	2	Q9WA16	Q9WA16 hepatitis c
451	6	2.7	42	2	Q8JPF3	Q8JPF3 hepatitis c	524	6	2.7	82	2	Q29354	Q29354 sus scrofa
452	6	2.7	43	2	Q6D110	Q6D110 erwinia car	525	6	2.7	82	2	Q8XU57	Q8XU57 ralatonia s
453	6	2.7	45	2	Q92A35	Q92A35 listeria in	526	6	2.7	82	2	Q4514	Q4514 paramascium
454	6	2.7	45	2	Q8Y5S5	Q8Y5S5 listeria mo	527	6	2.7	83	2	Q6C213	Q6C213 yarrowia li
455	6	2.7	47	2	Q841Q9	Q841Q9 frankia sp.	528	6	2.7	84	1	OAG1_SALTY	OAG1_SALTY salmonella
456	6	2.7	47	2	Q9WT97	Q9WT97 hepatitis c	529	6	2.7	85	1	GON2_HAPRU	GON2_HAPRU pyrogococ
457	6	2.7	49	2	Q7RRV1	Q7RRV1 plasmodium	530	6	2.7	85	2	Q8U2K1	Q8U2K1 pyrogococ
458	6	2.7	50	2	Q9PSQ4	Q9PSQ4 gallus gall	531	6	2.7	85	2	Q7V6X6	Q7V6X6 prochloroco
459	6	2.7	54	2	Q879Q2	Q879Q2 streptococ	532	6	2.7	85	2	Q76FQ2	Q76FQ2 oreochromis
460	6	2.7	54	2	Q9A1S7	Q9A1S7 streptococ	533	6	2.7	85	2	AAC27717	AAC27717 haplochrom
461	6	2.7	54	2	Q8VSG4	Q8VSG4 shigella fl	534	6	2.7	85	2	BAC65155	BAC65155 oreochrom
462	6	2.7	57	2	Q8LKH8	Q8LKH8 lolium pere	535	6	2.7	85	2	BAC56850	BAC56850 oreochrom
463	6	2.7	57	2	Q7YWL5	Q7YWL5 lumbricus t	536	6	2.7	86	2	Q7XIZ2	Q7XIZ2 oryza sativ
464	6	2.7	58	2	Q7UA64	Q7UA64 synecococc	537	6	2.7	86	2	Q8ZFO0	Q8ZFO0 versinia pe
465	6	2.7	58	2	Q9DIM4	Q9DIM4 hepatitis c	538	6	2.7	86	2	BAC82912	BAC82912 oryza eat
466	6	2.7	58	2	Q9DIM5	Q9DIM5 hepatitis c	539	6	2.7	86	2	AAS62000	AAS62000 versinia
467	6	2.7	58	2	Q9DIM6	Q9DIM6 hepatitis c	540	6	2.7	88	2	Q77WZ7	Q77WZ7 hepatitis c
468	6	2.7	58	2	Q9DIQ0	Q9DIQ0 hepatitis c	541	6	2.7	88	2	Q77WZ8	Q77WZ8 hepatitis c
469	6	2.7	58	2	Q9DIQ1	Q9DIQ1 hepatitis c	542	6	2.7	88	2	Q9W887	Q9W887 hepatitis c

543	6	2.7	89	2	Q6VTG3	Q6vtg3 oryza sativ	616	6	2.7	103	2	BAC98573	Bac98573 oryza sat
544	6	2.7	89	2	BAD17766	Bad17766 oryza sat	617	6	2.7	103	2	BAC99714	Bac99714 oryza sat
545	6	2.7	89	2	BAD17774	Bad17774 oryza sat	618	6	2.7	104	1	HSP2_RAT	Pl1248 rattus norv
546	6	2.7	90	2	Q77677	Q77677 sus scrofa	619	6	2.7	104	2	Q72250	Q72260 hepatitis c
547	6	2.7	90	2	Q77UTX5	Q77utx5 rhodopirell	620	6	2.7	104	2	Q84192	Q84192 newcastle d
548	6	2.7	90	2	Q98UD9	Q98jd9 rhizobium l	621	6	2.7	104	2	Q9WJ27	Q9wj27 newcastle d
549	6	2.7	91	2	Q76LQ2	Q76lq2 haemaphysal	622	6	2.7	105	1	HSP2_RATFU	Q9wfe9 xylella fas
550	6	2.7	91	2	Q82965	Q82965 ralestonia s	623	6	2.7	105	2	Q9PF9	Q72261 hepatitis c
551	6	2.7	91	2	Q8XFW3	Q8xpw3 ralestonia s	624	6	2.7	105	2	Q72261	Q72261 hepatitis c
552	6	2.7	91	2	Q92980	Q92980 hepatitis c	625	6	2.7	106	2	Q6WPI1	Q6wp11 atthis helo
553	6	2.7	91	2	Q77PM5	Q77pm5 hepatitis c	626	6	2.7	106	2	Q82U69	Q82u69 nitrosonona
554	6	2.7	91	2	Q77PM6	Q77pm6 hepatitis c	627	6	2.7	106	2	Q72254	Q72254 hepatitis c
555	6	2.7	91	2	Q77PM7	Q77pm7 hepatitis c	628	6	2.7	106	2	Q72255	Q72255 hepatitis c
556	6	2.7	91	2	Q77PM8	Q77pm8 hepatitis c	629	6	2.7	106	2	Q72256	Q72256 hepatitis c
557	6	2.7	91	2	Q77PM5	Q77pm5 hepatitis c	630	6	2.7	106	2	Q72257	Q72257 hepatitis c
558	6	2.7	91	2	Q9W8F6	Q9w8f6 hepatitis c	631	6	2.7	106	2	AAQ92070	AAQ92070 atthis he
559	6	2.7	91	2	Q9W8M5	Q9w8m5 hepatitis c	632	6	2.7	107	2	Q935B2	Q935b2 salmonella
560	6	2.7	91	2	Q9WN25	Q9wn25 hepatitis c	633	6	2.7	108	2	Q81ZD3	Q81zdz3 anabaena sp
561	6	2.7	91	2	Q9WN26	Q9wn26 hepatitis c	634	6	2.7	108	2	Q9QW50	Q9qw50 peromyscus
562	6	2.7	91	2	Q9WN27	Q9wn27 hepatitis c	635	6	2.7	109	2	Q9FTD3	Q9ftd3 oryza sativ
563	6	2.7	91	2	Q9WN29	Q9wn29 hepatitis c	636	6	2.7	110	2	Q8ZSN0	Q8zsn0 pyrobaculum
564	6	2.7	91	2	Q9WN38	Q9wn38 hepatitis c	637	6	2.7	110	2	Q6BVT8	Q6bvt8 debaryomyce
565	6	2.7	91	2	BAD03393	Bad0393 haemaphys	638	6	2.7	110	2	Q86YL1	Q86yl1 homo sapien
566	6	2.7	92	2	Q6BJ99	Q6bj99 debaryomyce	639	6	2.7	112	2	Q70ZA7	Q70za7 canis faml
567	6	2.7	92	2	Q9P0G2	Q9p0g2 homo sapien	640	6	2.7	112	2	Q6WPH8	Q6wph8 cosiligena t
568	6	2.7	93	2	Q87EE4	Q87ee4 xylella fas	641	6	2.7	112	2	Q6WPH9	Q6wph9 calothorax
569	6	2.7	93	2	Q82U33	Q82u33 rhizobium m	642	6	2.7	112	2	Q6WPI0	Q6wpi0 selasphorus
570	6	2.7	93	2	Q9WUZ6	Q9wuz6 m thymus an	643	6	2.7	112	2	Q6WPI2	Q6wpi2 lampornis v
571	6	2.7	93	2	Q9ERE0	Q9ere0 rattus norv	644	6	2.7	112	2	Q6WPI3	Q6wpi3 glaucidium
572	6	2.7	93	2	Q72259	Q72259 hepatitis c	645	6	2.7	112	2	Q6WPI5	Q6wpi5 collocalia
573	6	2.7	94	2	Q6HPC8	Q6hpc8 bacillus th	646	6	2.7	112	2	Q6WPI6	Q6wpi6 streptococ
574	6	2.7	94	2	Q9F568	Q9f568 escherichia	647	6	2.7	112	2	Q6WPI7	Q6wpi7 geococcyx v
575	6	2.7	94	2	Q73ES0	Q73es0 bacillus ce	648	6	2.7	112	2	Q6WPI8	Q6wpi8 micrathene
576	6	2.7	94	2	Q81VE2	Q81ve2 bacillus an	649	6	2.7	112	2	Q6WPI9	Q6wpi9 nyctiphrynu
577	6	2.7	94	2	AA539224	Aa539224 bacillus	650	6	2.7	112	2	Q6WPI0	Q6wpi0 caprimulgus
578	6	2.7	94	2	AA129349	Aa129349 bacillus	651	6	2.7	112	2	Q6WPI1	Q6wpi1 trogon meia
579	6	2.7	95	2	Q6YQB4	Q6yqb4 onion yello	652	6	2.7	112	2	Q6WPI2	Q6wpi2 trogon citr
580	6	2.7	95	2	BAD04546	Bad04546 onion yel	653	6	2.7	112	2	Q6WPI3	Q6wpi3 sphyrapicus
581	6	2.7	97	2	Q7NXU9	Q7nxu9 chromobacte	654	6	2.7	112	2	Q6WPI5	Q6wpi5 motomus mex
582	6	2.7	97	2	Q7V728	Q7v728 prochloroco	655	6	2.7	112	2	Q6WPI6	Q6wpi6 pionus seni
583	6	2.7	97	2	Q9HY51	Q9hy51 pseudomonas	656	6	2.7	112	2	CAD24218	Cad24218 canis fam
584	6	2.7	98	2	Q8FSJ6	Q8fsj6 corynebacte	657	6	2.7	112	2	AAQ92055	AAQ92055 pionus se
585	6	2.7	98	2	Q9DGL8	Q9dgl8 gallus gall	658	6	2.7	112	2	AAQ92056	AAQ92056 motomus m
586	6	2.7	99	2	Q9HWP0	Q9hwp0 pseudomonas	659	6	2.7	112	2	AAQ92057	AAQ92057 sphyrapic
587	6	2.7	99	2	Q70V42	Q70v42 cyprinus ca	660	6	2.7	112	2	AAQ92059	AAQ92059 trogon ci
588	6	2.7	99	2	CAD59917	Cad59917 cyprinus	661	6	2.7	112	2	AAQ92060	AAQ92060 trogon me
589	6	2.7	100	1	URE3_PROVM	Q7v3v4 prochloroco	662	6	2.7	112	2	AAQ92061	AAQ92061 caprimulg
590	6	2.7	100	1	URE3_SYNPN	Q8f400 synchococc	663	6	2.7	112	2	AAQ92062	AAQ92062 nyctiphry
591	6	2.7	100	1	URE3_SYNPNX	Q7u315 synchococc	664	6	2.7	112	2	AAQ92063	AAQ92063 micrathen
592	6	2.7	100	2	Q9G8C3	Q9g8c3 sheppardia	665	6	2.7	112	2	AAQ92064	AAQ92064 geococcyx
593	6	2.7	100	2	Q53718	Q53718 streptomyce	666	6	2.7	112	2	AAQ92065	AAQ92065 streptopr
594	6	2.7	100	2	Q8DG82	Q8dg82 synchococc	667	6	2.7	112	2	AAQ92066	AAQ92066 collocali
595	6	2.7	100	2	Q91652	Q91652 pseudomonas	668	6	2.7	112	2	AAQ92068	AAQ92068 glaucidiu
596	6	2.7	100	2	Q8K351	Q8k351 mus musculu	669	6	2.7	112	2	AAQ92069	AAQ92069 lampornis
597	6	2.7	101	2	Q6WPI4	Q6wpi4 apus apus (670	6	2.7	112	2	AAQ92071	AAQ92071 selasphor
598	6	2.7	101	2	Q952Q4	Q952q4 euphorbia p	671	6	2.7	112	2	AAQ92072	AAQ92072 calothora
599	6	2.7	101	2	Q8RVPY7	Q8rvy7 allium cepa	672	6	2.7	112	2	AAQ92073	AAQ92073 coeligena
600	6	2.7	101	2	Q7P1N8	Q7pin8 chromobacte	673	6	2.7	113	2	Q8MRZ1	Q8mrz1 drosophila
601	6	2.7	101	2	Q77WZ4	Q77wz4 hepatitis c	674	6	2.7	113	2	Q9G176	Q9g176 sheppardia
602	6	2.7	101	2	Q9W947	Q9w947 hepatitis c	675	6	2.7	113	2	Q9G212	Q9g212 sheppardia
603	6	2.7	101	2	AAQ92067	AAQ92067 apus apus	676	6	2.7	113	2	Q9G2F2	Q9g2f2 sheppardia
604	6	2.7	102	2	Q93UM3	Q93um3 synchococc	677	6	2.7	113	2	Q9G8C4	Q9g8c4 sheppardia
605	6	2.7	102	2	Q73NN6	Q73nn6 treponema d	678	6	2.7	113	2	Q9G8C5	Q9g8c5 sheppardia
606	6	2.7	102	2	Q7UMM6	Q7umm6 rhodopirell	679	6	2.7	113	2	Q9G8C6	Q9g8c6 sheppardia
607	6	2.7	102	2	Q9X868	Q9x868 streptomyce	680	6	2.7	113	2	Q9G8C7	Q9g8c7 sheppardia
608	6	2.7	102	2	Q8C2B7	Q8c2b7 mus musculu	681	6	2.7	113	2	Q9G8C8	Q9g8c8 sheppardia
609	6	2.7	102	2	Q9D8U9	Q9d8u9 m mus muscu	682	6	2.7	113	2	Q9G8C9	Q9g8c9 sheppardia
610	6	2.7	102	2	Q72263	Q72263 hepatitis c	683	6	2.7	113	2	Q9G8D0	Q9g8d0 sheppardia
611	6	2.7	102	2	Q92981	Q92981 hepatitis c	684	6	2.7	113	2	Q9G8D1	Q9g8d1 sheppardia
612	6	2.7	102	2	AA511605	Aa511605 treponema	685	6	2.7	113	2	Q9G8D2	Q9g8d2 sheppardia
613	6	2.7	103	2	Q6Z546	Q6z546 oryza sativ	686	6	2.7	113	2	Q9G8D3	Q9g8d3 sheppardia
614	6	2.7	103	2	Q8DF74	Q8df74 vibrio vuln	687	6	2.7	113	2	Q9XCB3	Q9xcb3 rhodothermu
615	6	2.7	103	2	Q806S9	Q806s9 hepatitis c	688	6	2.7	113	2	Q6D2F4	Q6d2f4 erwinia car

689	6	2.7	113	2	072289	072289 hepatitis c
690	6	2.7	114	2	Q8TPC5	Q8tpc5 methanosarc
691	6	2.7	114	2	Q8L482	Q8l482 oryza sativ
692	6	2.7	114	2	Q74CG1	Q74cgl geobacter s
693	6	2.7	114	2	AKR35090	Aar35090 geobacter
694	6	2.7	115	2	Q9LFS5	Q9lfs5 arabidopsis
695	6	2.7	116	2	Q6K3D0	Q6k3d0 oryza sativ
696	6	2.7	116	2	BAD22410	Bad22410 oryza sat
697	6	2.7	117	2	Q9YDG6	Q9ydg6 aeropyrum p
698	6	2.7	117	2	Q6SKY6	Q6sky6 speleonecte
699	6	2.7	117	2	Q9LHW6	Q9lhw6 oryza sativ
700	6	2.7	117	2	AA500887	Aa500887 speleonec
701	6	2.7	118	1	R18E_SULTO	Q96yw1 sulfolobus
702	6	2.7	118	2	P73674	P73674 synechocyst
703	6	2.7	118	2	Q9KBB6	Q9kbb6 bacillus ha
704	6	2.7	119	2	Q8DJ95	Q8dj95 synechococc
705	6	2.7	120	1	CLPS_PSESM	Q8rzs0 pseudomonas
706	6	2.7	120	2	Q9GB86	Q9gb86 rostratula
707	6	2.7	120	2	Q9GB87	Q9gb87 ireddiparra
708	6	2.7	120	2	Q9GB88	Q9gb88 microparra
709	6	2.7	120	2	Q9GB89	Q9gb89 metopidius
710	6	2.7	120	2	Q9GB90	Q9gb90 hydrophasia
711	6	2.7	120	2	Q9GB91	Q9gb91 jacara spin
712	6	2.7	120	2	Q9GB92	Q9gb92 jacara
713	6	2.7	120	2	Q9GB93	Q9gb93 actophilorn
714	6	2.7	120	2	Q9S557	Q9s557 pseudomonas
715	6	2.7	120	2	Q9KW33	Q9kw33 pseudomonas
716	6	2.7	120	2	Q8PFF0	Q8pff0 xanthomonas
717	6	2.7	120	2	Q8S565	Q8s565 pseudomonas
718	6	2.7	120	2	Q7DCU1	Q7dcj1 pseudomonas
719	6	2.7	120	2	Q72252	Q72252 hepatitis c
720	6	2.7	121	2	Q8ZVY4	Q8zvy4 pyrobaculum
721	6	2.7	121	2	Q8N950	Q8n950 homo sapien
722	6	2.7	121	2	Q82KC7	Q82kc7 streptomyce
723	6	2.7	121	2	Q8RVF6	Q8rvf6 deinococcus
724	6	2.7	121	2	Q9D9L9	Q9d9l9 mus musculu
725	6	2.7	121	2	Q72248	Q72248 hepatitis c
726	6	2.7	121	2	Q72250	Q72250 hepatitis c
727	6	2.7	121	2	Q72251	Q72251 hepatitis c
728	6	2.7	121	2	Q72253	Q72253 hepatitis c
729	6	2.7	121	2	Q72264	Q72264 hepatitis c
730	6	2.7	121	2	Q72265	Q72265 hepatitis c
731	6	2.7	121	2	Q72266	Q72266 hepatitis c
732	6	2.7	121	2	Q72284	Q72284 hepatitis c
733	6	2.7	121	2	Q72285	Q72285 hepatitis c
734	6	2.7	121	2	Q72289	Q72289 hepatitis c
735	6	2.7	121	2	Q72291	Q72291 hepatitis c
736	6	2.7	121	2	Q72292	Q72292 hepatitis c
737	6	2.7	121	2	Q72293	Q72293 hepatitis c
738	6	2.7	121	2	Q72294	Q72294 hepatitis c
739	6	2.7	121	2	Q72295	Q72295 hepatitis c
740	6	2.7	121	2	Q72296	Q72296 hepatitis c
741	6	2.7	122	1	THIH_ORYSA	Q42443 oryza sativ
742	6	2.7	122	2	Q6K2X5	Q6k2x5 oryza sativ
743	6	2.7	122	2	Q7EZX7	Q7ezx7 oryza sativ
744	6	2.7	122	2	Q7WV00	Q7wv00 bordetella
745	6	2.7	122	2	Q7WBC0	Q7wbc0 bordetella
746	6	2.7	122	2	Q7WMT9	Q7wmt9 bordetella
747	6	2.7	122	2	Q92EV2	Q92ev2 listeria in
748	6	2.7	122	2	BAC79928	Bac79928 oryza sat
749	6	2.7	122	2	BAD20012	Bad20012 oryza sat
750	6	2.7	123	2	Q8GFT7	Q8gft7 pseudomonas
751	6	2.7	123	2	Q6NA83	Q6na83 rhodopseudo
752	6	2.7	123	2	CAE26745	Ca26745 rhodopseu
753	6	2.7	124	1	WFD2_CANFA	Q28894 canis fami
754	6	2.7	124	2	Q9PKS3	Q9pks3 chlamydia m
755	6	2.7	125	2	Q8U270	Q8u270 pyrococcus
756	6	2.7	125	2	Q8IQI8	Q8iqi8 drosophila
757	6	2.7	125	2	Q7NGE6	Q7nge6 gloeobacter
758	6	2.7	125	2	Q8DUU9	Q8duu9 streptococc
759	6	2.7	126	2	Q9VKE3	Q9vke3 drosophila
760	6	2.7	127	2	Q96M58	Q96m58 homo sapien
761	6	2.7	127	2	Q88H92	Q88h92 pseudomonas

Q86fb5	schistosoma	128	2	Q86FB5	Q86fb5 schistosoma
Q72ja7	thermus	128	2	Q72JA7	Q72ja7 thermus
Q8g6x6	bifidobacte	128	2	Q8G6X6	Q8g6x6 bifidobacte
Aa81216	thermus t	128	2	AAS81216	Aa81216 thermus t
Q9xf14	zea mays (m	129	2	Q9XF14	Q9xf14 zea mays (m
P74748	synechocyst	129	2	P74748	P74748 synechocyst
Q8ck94	yersinia pe	129	2	Q8CK94	Q8ck94 yersinia pe
Q8c924	mus musculu	129	2	Q8C924	Q8c924 mus musculu
Aa60429	yersinia	129	2	AAS60429	Aa60429 yersinia
Q7eyul	oryza sativ	129	2	Q7EYU1	Q7eyul oryza sativ
Q7nsf8	chromobacte	130	2	Q7NSF8	Q7nsf8 chromobacte
Q8be71	mus musculu	130	2	Q8BS71	Q8be71 mus musculu
Bac84193	oryza eat	130	2	BAC84193	Bac84193 oryza eat
P94143	wautersia m	131	2	P94143	P94143 wautersia m
Q8buc5	mus musculu	131	2	Q8BUC5	Q8buc5 mus musculu
Q92043	mus musculu	131	2	Q9R043	Q92043 mus musculu
P27114	oryctolagus	133	1	MOTI_RABIT	P27114 oryctolagus
Q91dp2	sapporo vir	133	2	Q91DP2	Q91dp2 sapporo vir
Q91dr7	sapporo vir	133	2	Q91DR7	Q91dr7 sapporo vir
O34035	streptococc	134	2	O34035	O34035 streptococc
Q72b49	thermus the	134	2	Q72H49	Q72b49 thermus the
Q68191	hepatitis c	134	2	Q68191	Q68191 hepatitis c
Aa81988	thermus t	134	2	AAS81988	Aa81988 thermus t
Q7sg61	neurospora	135	2	Q7SG61	Q7sg61 neurospora
Q9zli7	helicobacte	135	2	Q9ZLI7	Q9zli7 helicobacte
Q68190	hepatitis c	135	2	Q68190	Q68190 hepatitis c
P30059	epifagus vi	136	1	RE11_EPIVI	P30059 epifagus vi
Q83v7	anaplasma p	136	2	Q83V77	Q83v7 anaplasma p
Q8vgi6	uncultured	136	2	Q8VQI6	Q8vgi6 uncultured
P09697	human cytom	137	1	US33_HCMVA	P09697 human cytom
Q9p4y2	neurospora	137	2	Q9P4Y2	Q9p4y2 neurospora
Q6lxf8	methanococc	138	2	Q6LXF8	Q6lxf8 methanococc
Q7p728	fusobacteri	138	2	Q7P728	Q7p728 fusobacteri
Q6lip2	photobacter	138	2	Q6LIP2	Q6lip2 photobacter
Cal3049	methanoco	138	2	CAL3049	Cal3049 methanoco
Cag22838	photobact	138	2	CAG22838	Cag22838 photobact
P43981	haemophilus	139	1	RUUV_HAEIN	P43981 haemophilus
Q9U9A2	leishmania	139	2	Q9U9A2	Q9U9A2 leishmania
Q6ygf7	onion yello	139	2	Q6YQF7	Q6ygf7 onion yello
Ba04501	onion yel	139	2	BAD04501	Ba04501 onion yel
Q6k5h2	oryza sativ	140	2	Q6K5H2	Q6k5h2 oryza sativ
Q69479	mycobacteri	140	2	Q69479	Q69479 mycobacteri
Q7uu6	rhodopirell	140	2	Q7UUU6	Q7uu6 rhodopirell
Bad22153	oryza sat	140	2	BAD22153	Bad22153 oryza sat
O34762	bacillus su	141	1	OHRA_BACSU	O34762 bacillus su
Q7gm43	anopheles g	141	2	Q7QMA3	Q7gm43 anopheles g
Q8f0e7	pseudomonas	141	2	Q8F0E7	Q8f0e7 pseudomonas
Q8cjt5	gnetum ghem	142	2	Q8CTJ5	Q8cjt5 gnetum ghem
Q87y13	pseudomonas	142	2	Q87Y13	Q87y13 pseudomonas
Q8rvr4	oryza sativ	143	2	Q8RVR4	Q8rvr4 oryza sativ
Q8s3l2	populus tre	143	2	Q8S3L2	Q8s3l2 populus tre
Q74f82	geobacter s	143	2	Q74F82	Q74f82 geobacter s
Q8fnk3	corynebacte	143	2	Q8FNK3	Q8fnk3 corynebacte
Aar34057	geobacter	143	2	AAR34057	Aar34057 geobacter
Q8tyk1	methanopyru	144	2	Q8TYK1	Q8tyk1 methanopyru
Q6ldd4	xanthomonas	144	2	Q6LDD4	Q6ldd4 xanthomonas
Q7urr2	rhodopirell	144	2	Q7URR2	Q7urr2 rhodopirell
Q7uw02	rhodopirell	144	2	Q7UW02	Q7uw02 rhodopirell
Q8p498	xanthomonas	144	2	Q8P498	Q8p498 xanthomonas
Q8pfv5	xanthomonas	144	2	Q8PFV5	Q8pfv5 xanthomonas
Aab19435	xanthomon	144	2	AAB19435	Aab19435 xanthomon
Q6l2w8	picrophilus	145	2	Q6L2W8	Q6l2w8 picrophilus
Q6ml20	bdellovibri	145	2	Q6ML20	Q6ml20 bdellovibri
Ca80037	bdellovibri	145	2	CAE80037	Ca80037 bdellovibri
Q7phd9	anopheles g	146	2	Q7PHD9	Q7phd9 anopheles g
Q9xaa2	streptocomye	146	2	Q9XAA2	Q9xaa2 streptocomye
Q73yg4	mycobacteri	147	2	Q73YG4	Q73yg4 mycobacteri
Aa804309	mycobacte	147	2	AAS04309	Aa804309 mycobacte
P07492	homo sapien	148	1	GRP_HUMAN	P07492 homo sapien
Q97bg5	thermoplasm	148	2	Q97BG5	Q97bg5 thermoplasm
Q8lp66	drosophila	148	2	Q8IP66	Q8lp66 drosophila
Q9gmxl	macaca fasc	148	2	Q9GMX1	Q9gmxl macaca fasc

981 1 MFT ARATH 1 173 2.7 6 Q9xfk7 arabidopsis 1054 188 2 Q8u3k9 pyrococcus
982 2 Q9YE66 2 173 2.7 6 Q9c2b5 nausporas
983 2 Q6L5N9 2 173 2.7 6 Q8d231 gloebacter
984 2 Q75QW9 2 173 2.7 6 Q88j33 pseudomonas
985 2 Q841P7 2 173 2.7 6 Q88j33 pseudomonas
986 2 Q841Q1 2 173 2.7 6 P03608 turnip yell
987 2 Q841P7 2 173 2.7 6 P20125 turnip yell
988 2 Q841Q1 2 173 2.7 6 Q8zu1 pyrrobaculum
989 2 Q841Q1 2 173 2.7 6 Q86qv2 homo sapien
990 2 Q841Q1 2 173 2.7 6 Q7xw10 oryza sativ
991 2 Q841Q1 2 173 2.7 6 Q9yq2 onion yello
992 2 Q841Q1 2 173 2.7 6 Q7ncm7 gloebacter
993 2 Q841Q1 2 173 2.7 6 Q7uly6 deinococcus
994 2 Q841Q1 2 173 2.7 6 Q9rtls rhodospirell
995 2 Q841Q1 2 173 2.7 6 P90242 turnip yell
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999 2 Q841Q1 2 173 2.7 6 Aab49374 turnip yell
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1004 2 Q841Q1 2 173 2.7 6 Aaq23784 hepatitis c
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1006 2 Q841Q1 2 173 2.7 6 P22728 gallus gall
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1009 2 Q841Q1 2 173 2.7 6 Q7z4r8 homo sapien
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1011 2 Q841Q1 2 173 2.7 6 Q7rfv8 plasmodium
1012 2 Q841Q1 2 173 2.7 6 Q8ss22 encephalito
1013 2 Q841Q1 2 173 2.7 6 Q46673 escherichia
1014 2 Q841Q1 2 173 2.7 6 Q6vdx3 hepatitis c
1015 2 Q841Q1 2 173 2.7 6 Q6vdx4 hepatitis c
1016 2 Q841Q1 2 173 2.7 6 Q6vdx8 hepatitis c
1017 2 Q841Q1 2 173 2.7 6 Q8bbk1 hepatitis c
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1020 2 Q841Q1 2 173 2.7 6 Q8jpg2 hepatitis c
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1022 2 Q841Q1 2 173 2.7 6 Q8jpg5 hepatitis c
1023 2 Q841Q1 2 173 2.7 6 Q8jpg6 hepatitis c
1024 2 Q841Q1 2 173 2.7 6 Q8jpg7 hepatitis c
1025 2 Q841Q1 2 173 2.7 6 Aaq23786 hepatitis c
1026 2 Q841Q1 2 173 2.7 6 Aaq23790 hepatitis c
1027 2 Q841Q1 2 173 2.7 6 Aaq23791 hepatitis c
1028 2 Q841Q1 2 173 2.7 6 Q87703 aquifex aeo
1029 2 Q841Q1 2 173 2.7 6 Q83183 treponema p
1030 2 Q841Q1 2 173 2.7 6 Q7riy9 plasmodium
1031 2 Q841Q1 2 173 2.7 6 Q8ijs2 plasmodium
1032 2 Q841Q1 2 173 2.7 6 Q8h2v1 oryza sativ
1033 2 Q841Q1 2 173 2.7 6 Q7n527 photorhabdu
1034 2 Q841Q1 2 173 2.7 6 Q8kaa4 bacillus ha
1035 2 Q841Q1 2 173 2.7 6 Q6vdx0 hepatitis c
1036 2 Q841Q1 2 173 2.7 6 Q6vdx1 hepatitis c
1037 2 Q841Q1 2 173 2.7 6 Q6vdx2 hepatitis c
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1046 2 Q841Q1 2 173 2.7 6 Aaq23793 hepatitis c
1047 2 Q841Q1 2 173 2.7 6 Aaq23794 hepatitis c
1048 2 Q841Q1 2 173 2.7 6 Q96ee9 homo sapien
1049 2 Q841Q1 2 173 2.7 6 Q84zf1 oryza sativ
1050 2 Q841Q1 2 173 2.7 6 Q8e967 shewanella
1051 2 Q841Q1 2 173 2.7 6 Q8ftk9 corynebacte
1052 2 Q841Q1 2 173 2.7 6 Q8pdy9 xanthomonas
1053 2 Q841Q1 2 173 2.7 6 Q6vdx7 hepatitis c
Aar35129 geobacter

Q9xfk7 arabidopsis 1054
Q9ve66 aeropyrum p 1055
Q6l5n9 populus nig 1056
Q75q9w populus nig 1057
Q841p7 anaplasm p 1058
Q841q1 anaplasm p 1059
Bad08339 populus n 1060
Q6zwl2 homo sapien 1061
Q8as11 oryza sativ 1062
Q8gnf9 erlichia c 1063
Q6d0d7 erwinia car 1064
Q69999 streptomyce 1065
Bac85695 homo sapi 1066
Q9zyy0 hippopotamu 1067
Q6bs90 debaryomyce 1068
Q84pu4 oryza sativ 1069
Q7nl54 photorhabdu 1070
Q8zd43 yersinia pe 1071
Q54195 streptomyce 1072
Q63613 rattus norv 1073
Q95it4 arabidopsis 1074
Q877d7 pyrobaculum 1075
Q8t378 lumbricus t 1076
Q7v873 rickettsia 1077
Q9zdm3 rickettsia 1078
Q84x11 lycopersico 1079
Q9k1j5 streptomyce 1080
Q81aa9 bacillus ce 1081
Q8xm4 clostridium 1082
Q6fyc8 bartonella 1083
Q62740 rattus norv 1084
Q59788 schizosacch 1085
Q9hz84 pseudomonas 1086
Q9362 saccharomyc 1087
Q755c7 ashbya goss 1088
Q6f1j7 candida gla 1089
Q6cwq7 kluyveromyc 1090
Q9hcr8 homo sapien 1091
Q62956 oryza sativ 1092
Q7mqr5 wolinnella s 1093
Q83du4 coxiella bu 1094
Q809963 oryza sat 1095
Aas56385 saccharom 1096
Aas53270 ashbya go 1097
Q74bl2 geobacter s 1098
Q90y81 lampetra ja 1099
Aar35405 geobacter 1100
Q82868 rhodovulum 1101
Q9g8b7 loxodonta a 1102
Q9g8b8 elephas max 1103
Q9g8b9 elephas max 1104
Q9g8c0 elephas max 1105
Q9g8c1 elephas max 1106
Q9g8c2 elephas max 1107
Q84si8 raphanus sa 1108
Q701p4 pasteurella 1109
Q9cp51 pasteurella 1110
Cad92742 pasteurel 1111
O13954 schizosacch 1112
Q33984 saccharopol 1113
Q6bxz0 bacillus an 1114
Q75313 ashbya goss 1115
Q7ur38 rhodospirell 1116
Aas3670 ashbya go 1117
P42116 nausporas 1118
Q8wx15 homo sapien 1119
Q9niw6 leishmania 1120
Q6zf01 oryza sativ 1121
Q74cc2 geobacter s 1122
Q9dad3 m mus muscu 1123
Q8qrv4 chimpanzee 1124
Bac83430 oryza sat 1125
Aar35129 geobacter

1000 2 Q841Q1 2 173 2.7 6 Q8mif8 bdellovibri
1001 2 Q841Q1 2 173 2.7 6 Q89516 clostridium
1002 2 Q841Q1 2 173 2.7 6 Q8vdy0 hepatitis c
1003 2 Q841Q1 2 173 2.7 6 Aaq23784 hepatitis c
1004 2 Q841Q1 2 173 2.7 6 Ca80602 bdellovib
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1006 2 Q841Q1 2 173 2.7 6 Q9ybm4 aeropyrum p
1007 2 Q841Q1 2 173 2.7 6 Q96xm4 sulfobus
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1009 2 Q841Q1 2 173 2.7 6 Q96my2 homo sapien
1010 2 Q841Q1 2 173 2.7 6 Q7rfv8 plasmodium
1011 2 Q841Q1 2 173 2.7 6 Q8ss22 encephalito
1012 2 Q841Q1 2 173 2.7 6 Q46673 escherichia
1013 2 Q841Q1 2 173 2.7 6 Q6vdx3 hepatitis c
1014 2 Q841Q1 2 173 2.7 6 Q6vdx4 hepatitis c
1015 2 Q841Q1 2 173 2.7 6 Q6vdx8 hepatitis c
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1017 2 Q841Q1 2 173 2.7 6 Q8bbk2 hepatitis c
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1019 2 Q841Q1 2 173 2.7 6 Q8jpg2 hepatitis c
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1021 2 Q841Q1 2 173 2.7 6 Q8jpg5 hepatitis c
1022 2 Q841Q1 2 173 2.7 6 Q8jpg6 hepatitis c
1023 2 Q841Q1 2 173 2.7 6 Q8jpg7 hepatitis c
1024 2 Q841Q1 2 173 2.7 6 Aaq23786 hepatitis c
1025 2 Q841Q1 2 173 2.7 6 Aaq23790 hepatitis c
1026 2 Q841Q1 2 173 2.7 6 Aaq23791 hepatitis c
1027 2 Q841Q1 2 173 2.7 6 Q87703 aquifex aeo
1028 2 Q841Q1 2 173 2.7 6 Q83183 treponema p
1029 2 Q841Q1 2 173 2.7 6 Q7riy9 plasmodium
1030 2 Q841Q1 2 173 2.7 6 Q8ijs2 plasmodium
1031 2 Q841Q1 2 173 2.7 6 Q8h2v1 oryza sativ
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1052 2 Q841Q1 2 173 2.7 6 Q6vdx7 hepatitis c
1053 2 Q841Q1 2 173 2.7 6 Aar35129 geobacter

1127	6	2.7	194	1	FGF4 CHICK	P48804 gallus gall	1200	6	2.7	208	2	Q83455	Q83455 porcine ade
1128	6	2.7	194	2	Q7U655	Q7u655 synechococ	1201	6	2.7	208	2	Q8WER4	Q6wer4 molva molva
1129	6	2.7	195	2	Q8Wwx5	Q8wx5 homo sapien	1202	6	2.7	208	2	AAQ62777	AAQ62777 molva mol
1130	6	2.7	195	2	Q6SYD4	Q6syd4 nucella lam	1203	6	2.7	208	2	AAQ89059	AAQ89059 homo sapi
1131	6	2.7	195	2	Q7X1G2	Q7x1g2 leptospiril	1204	6	2.7	208	2	CAB581154	CAB581154 bdellovib
1132	6	2.7	195	2	Q91Z22	Q91z22 mus musculu	1205	6	2.7	209	2	Q972W3	Q972w3 sulfobobus
1133	6	2.7	195	2	AAK15876	AAK15876 nucella l	1206	6	2.7	209	2	Q6CF98	Q6cf98 yarrowia li
1134	6	2.7	196	2	Q91LT9	Q91lt9 pseudomonas	1207	6	2.7	209	2	Q8Wwx4	Q8wx4 homo sapien
1135	6	2.7	196	2	Q8XJTO	Q8xjto clostridium	1208	6	2.7	209	2	Q72UA1	Q72ua1 leptospira
1136	6	2.7	197	2	Q6CUM6	Q6cum6 kluyveromyc	1209	6	2.7	209	2	Q8FOT1	Q8fot1 leptospira
1137	6	2.7	197	2	Q7S265	Q7s265 homo sapien	1210	6	2.7	209	2	Q8YMX5	Q8ymx5 anabaena sp
1138	6	2.7	197	2	Q7PCG8	Q7pcg8 bacterioph	1211	6	2.7	209	2	Q8WERS	Q8wer5 broeme bros
1139	6	2.7	197	2	Q8LTF8	Q8ltf8 bacterioph	1212	6	2.7	209	2	Q9WPS6	Q9wps6 human immun
1140	6	2.7	197	2	Q79YD8	Q79yd8 streptococ	1213	6	2.7	209	2	AAQ62776	AAQ62776 broeme br
1141	6	2.7	197	2	Q8K6D6	Q8k6d6 streptococ	1214	6	2.7	209	2	AAQ62776	AAQ62776 broeme br
1142	6	2.7	197	2	Q8NZL2	Q8nzl2 streptococ	1215	6	2.7	209	2	AAQ62776	AAQ62776 broeme br
1143	6	2.7	197	2	Q8KXT6	Q8kxt6 streptococ	1216	6	2.7	210	2	Q82B37	Q82b37 streptococ
1144	6	2.7	197	2	Q99YA7	Q99ya7 streptococ	1217	6	2.7	211	1	UPP COREF	UPP COREF
1145	6	2.7	198	2	Q97V1	Q97v1 schizosacch	1218	6	2.7	211	2	Q7PKQ0	Q7pkq0 anopheles g
1146	6	2.7	198	2	Q89361	Q89361 paramedicu	1219	6	2.7	211	2	Q91118	Q91118 pseudomonas
1147	6	2.7	199	1	RS3A_PYRHO	RS3A_PYRHO	1220	6	2.7	211	2	Q98H93	Q98h93 rhizobium l
1148	6	2.7	199	2	Q91NL5	Q91nl5 arabidopsis	1221	6	2.7	211	2	Q8RA15	Q8ra15 thermotacoe
1149	6	2.7	199	2	Q33970	Q33970 streptococ	1222	6	2.7	211	2	Q6FCY2	Q6fcy2 acinetobact
1150	6	2.7	199	2	Q71110	Q71110 mus musculu	1223	6	2.7	211	2	Q91044	Q91044 human immun
1151	6	2.7	199	2	CAC83812	CAC83812 mus muscu	1224	6	2.7	211	2	Q91045	Q91045 human immun
1152	6	2.7	200	1	Y873_TREPA	Y873_TREPA	1225	6	2.7	211	2	Q9YPN6	Q9ypn6 human immun
1153	6	2.7	200	2	Q918E6	Q918e6 vibrio harv	1226	6	2.7	211	2	Q9YPN7	Q9ypn7 human immun
1154	6	2.7	200	2	Q32104	Q32104 bacillus su	1227	6	2.7	212	1	VF09_VACCC	VF09_VACCC
1155	6	2.7	200	2	Q8BNT3	Q8bnt3 mus musculu	1228	6	2.7	212	1	VF09_VACCV	VF09_VACCV
1156	6	2.7	200	2	Q7ZVR9	Q7zvr9 brachydantio	1229	6	2.7	212	1	VF09_VACCV	VF09_VACCV
1157	6	2.7	201	2	Q7WDA3	Q7wda3 vibrio vuln	1230	6	2.7	212	2	Q8BS89	Q8bs89 debaryomyce
1158	6	2.7	201	2	Q8CPX4	Q8cpx4 staphylococ	1231	6	2.7	212	2	Q9UAU4	Q9uau4 caenorhabdi
1159	6	2.7	201	2	Q8CYE6	Q8cy66 streptococ	1232	6	2.7	212	2	Q7XEX7	Q7xex7 oryza sativ
1160	6	2.7	201	2	Q8DFE0	Q8dfe0 vibrio vuln	1233	6	2.7	212	2	Q94I38	Q94i38 oryza sativ
1161	6	2.7	201	2	Q97P89	Q97p89 streptococ	1234	6	2.7	212	2	Q911E3	Q911e3 streptococ
1162	6	2.7	202	1	FTHC_HUMAN	FTHC_HUMAN	1235	6	2.7	212	2	Q8RZQ4	Q8rzq4 rabbitpox v
1163	6	2.7	202	1	NURM_TRYBB	NURM_TRYBB	1236	6	2.7	212	2	Q76Q41	Q76q41 variola min
1164	6	2.7	202	2	Q8N8X8	Q8n8x8 homo sapien	1237	6	2.7	212	2	Q76QL2	Q76ql2 cowpox viru
1165	6	2.7	202	2	Q7W4X4	Q7w4x4 bordetella	1238	6	2.7	212	2	Q76ZW7	Q76zw7 vaccinia vi
1166	6	2.7	203	1	SP24_MOUSE	SP24_MOUSE	1239	6	2.7	212	2	Q775Z1	Q775z1 camelpox vi
1167	6	2.7	203	2	Q6LOV8	Q6lov8 picophilus	1240	6	2.7	212	2	Q77TM9	Q77tm9 vaccinia vi
1168	6	2.7	203	2	Q8Q011	Q8q011 methanosarc	1241	6	2.7	212	2	Q8JLH2	Q8jlh2 ectromelia
1169	6	2.7	203	2	Q8TLH1	Q8tlh1 methanosarc	1242	6	2.7	212	2	Q9PXR7	Q9pxr7 variola vir
1170	6	2.7	203	2	Q6Z979	Q6z979 oryza sativ	1243	6	2.7	212	2	Q8QN09	Q8qn09 cowpox viru
1171	6	2.7	203	2	Q7NQZ1	Q7nqz1 chromobacte	1244	6	2.7	212	2	Q8V2X3	Q8v2x3 camelpox v
1172	6	2.7	203	2	Q6LRV4	Q6lr4 photobacter	1245	6	2.7	212	2	Q8V539	Q8v539 monkeypox v
1173	6	2.7	203	2	BAD01748	BAD01748 oryza sat	1246	6	2.7	212	2	AAK33900	AAK33900 vaccinia
1174	6	2.7	203	2	BAD03386	BAD03386 oryza sat	1247	6	2.7	212	2	CAB54633	CAB54633 variola m
1175	6	2.7	203	2	CAG19972	CAG19972 photobact	1248	6	2.7	212	2	AAO89327	AAO89327 vaccinia
1176	6	2.7	204	2	Q9HSG4	Q9hsg4 halobacteri	1249	6	2.7	212	2	AAAB96419	AAAB96419 vaccinia
1177	6	2.7	204	2	Q7QH61	Q7qh61 anophelies g	1250	6	2.7	212	2	CAD90597	CAD90597 cowpox vi
1178	6	2.7	204	2	Q8SU66	Q8su66 encephalito	1251	6	2.7	212	2	AAK49750	AAK49750 rabbitpox
1179	6	2.7	204	2	Q8LR35	Q8lr35 oryza sativ	1252	6	2.7	212	2	AAK10436	AAK10436 vaccinia
1180	6	2.7	205	2	Q29223	Q29223 archaeoglob	1253	6	2.7	213	2	Q5Z914	Q5z914 oryza sativ
1181	6	2.7	205	2	Q8JTB3	Q8jtb3 methanosarc	1254	6	2.7	213	2	Q7D766	Q7d766 mycobacteri
1182	6	2.7	205	2	Q9BLF3	Q9blf3 entamoeba h	1255	6	2.7	213	2	Q877V3	Q877v3 xylella fas
1183	6	2.7	205	2	Q91LBV6	Q91lbv6 streptococ	1256	6	2.7	213	2	Q88P58	Q88p58 pseudomonas
1184	6	2.7	206	2	Q7RYM3	Q7rym3 neurospora	1257	6	2.7	213	2	Q9PCS8	Q9pcs8 xylella fas
1185	6	2.7	206	2	Q7XGS8	Q7xgs8 oryza sativ	1258	6	2.7	213	2	Q9PD10	Q9pd10 xylella fas
1186	6	2.7	206	2	Q94H15	Q94h15 oryza sativ	1259	6	2.7	213	2	Q8BJJ1	Q8bjj1 mus musculu
1187	6	2.7	206	2	Q9RW3	Q9rw3 deinococcus	1260	6	2.7	213	2	Q8R014	Q8r014 m bsp-like
1188	6	2.7	206	2	Q9KZV1	Q9kzv1 streptococ	1261	6	2.7	213	2	BAD09883	BAD09883 oryza sat
1189	6	2.7	207	2	Q81YH0	Q81yh0 homo sapien	1262	6	2.7	214	1	RNFG_PSEAE	RNFG_PSEAE
1190	6	2.7	207	2	Q9H8A1	Q9h8a1 homo sapien	1263	6	2.7	214	2	Q9BX73	Q9bx73 homo sapien
1191	6	2.7	207	2	Q21466	Q21466 mytilus cal	1264	6	2.7	214	2	Q8VYV2	Q8vyv2 daucus caro
1192	6	2.7	207	2	Q9KVQ5	Q9kvq5 vibrio chol	1265	6	2.7	215	2	Q8D7H1	Q8d7h1 erwinia car
1193	6	2.7	207	2	Q72639	Q72639 human immun	1266	6	2.7	216	2	Q8AX66	Q8ax66 brachydantio
1194	6	2.7	208	2	Q81WS2	Q81ws2 homo sapien	1267	6	2.7	218	1	IFEI_MAIZE	IFEI_MAIZE
1195	6	2.7	208	2	Q8N131	Q8n131 homo sapien	1268	6	2.7	218	1	TRPF_BACHD	TRPF_BACHD
1196	6	2.7	208	2	Q7QV92	Q7qv92 giardia lam	1269	6	2.7	218	2	Q7WGF2	Q7wgf2 bordetella
1197	6	2.7	208	2	Q85MP0	Q85mp0 simillium ve	1270	6	2.7	218	2	Q8DGM1	Q8dgm1 synechococ
1198	6	2.7	208	2	Q6MGX5	Q6mgx5 bdellovibri	1271	6	2.7	218	2	Q8NU70	Q8nu70 corynebacte
1199	6	2.7	208	2	Q82LK0	Q82lk0 streptococ	1272	6	2.7	218	2	Q8BT62	Q8bt62 mus musculu

1273	6	2.7	218	2	CAP18637	Caf18637 corynebact	1346	6	2.7	228	2	Q950J8	Q950J8 amnospermop
1274	6	2.7	219	1	CPY1_YEAST	P14306 saccharomyc	1347	6	2.7	228	2	Q748P3	Q748P3 geobacter s
1275	6	2.7	219	2	Q8LBM6	Q8LBM6 arabidopsis	1348	6	2.7	228	2	Q7NGS5	Q7NGS5 gloebacter
1276	6	2.7	219	2	Q9ZSC7	Q9ZSC7 ipomoea bat	1349	6	2.7	228	2	Q8B3X7	Q8B3X7 porcine lym
1277	6	2.7	219	2	Q9FIE4	Q9FIE4 arabidopsis	1350	6	2.7	228	2	AAR36350	AAR36350 geobacter
1278	6	2.7	219	2	Q740S7	Q740S7 mycobacteri	1351	6	2.7	229	2	Q94N59	Q94N59 amnospermop
1279	6	2.7	219	2	Q9A261	Q9A261 caulobacter	1352	6	2.7	229	2	Q950I9	Q950I9 amnospermop
1280	6	2.7	219	2	Q90XR7	Q90XR7 brachydanio	1353	6	2.7	229	2	Q950J1	Q950J1 amnospermop
1281	6	2.7	219	2	AAS03582	AAS03582 mycobacte	1354	6	2.7	229	2	Q950K1	Q950K1 amnospermop
1282	6	2.7	220	2	Q9E284	Q9E284 acanthinuce	1355	6	2.7	229	2	Q9CFK1	Q9CFK1 lactococcus
1283	6	2.7	220	2	Q6MHS9	Q6MHS9 bdellovibri	1356	6	2.7	229	2	Q8Y394	Q8Y394 raistonia s
1284	6	2.7	220	2	Q82BH6	Q82BH6 streptomyce	1357	6	2.7	230	2	Q8TQZ7	Q8TQZ7 pyrococcus
1285	6	2.7	220	2	Q89JU3	Q89JU3 bradyrhizob	1358	6	2.7	230	2	Q94ND2	Q94ND2 amnospermop
1286	6	2.7	220	2	Q810M0	Q810M0 mus musculu	1359	6	2.7	230	2	Q94NK9	Q94NK9 amnospermop
1287	6	2.7	220	2	CAE78253	CAE78253 bdellovib	1360	6	2.7	230	2	Q94P19	Q94P19 amnospermop
1288	6	2.7	221	2	Q6SMZ7	Q6SMZ7 aotus azara	1361	6	2.7	230	2	Q950I8	Q950I8 amnospermop
1289	6	2.7	221	2	Q73WC0	Q73WC0 mycobacteri	1362	6	2.7	230	2	Q950J0	Q950J0 amnospermop
1290	6	2.7	221	2	Q8ETG6	Q8ETG6 oceanobacil	1363	6	2.7	230	2	Q950J3	Q950J3 amnospermop
1291	6	2.7	221	2	Q97H92	Q97H92 clostridium	1364	6	2.7	230	2	Q950J4	Q950J4 amnospermop
1292	6	2.7	221	2	AAR19667	AAR19667 aotus aza	1365	6	2.7	230	2	Q950J6	Q950J6 amnospermop
1293	6	2.7	221	2	AAS05057	AAS05057 mycobacte	1366	6	2.7	230	2	Q950J7	Q950J7 amnospermop
1294	6	2.7	222	2	Q6SN77	Q6SN77 cercocobus	1367	6	2.7	230	2	Q88R53	Q88R53 pseudomonas
1295	6	2.7	222	2	Q950J9	Q950J9 amnospermop	1368	6	2.7	231	2	Q92245	Q92245 magnaporthe
1296	6	2.7	222	2	Q40350	Q40350 mantoniella	1369	6	2.7	231	2	Q40332	Q40332 mantoniella
1297	6	2.7	222	2	AAR19587	AAR19587 cercocebu	1370	6	2.7	231	2	Q05483	Q05483 mantoniella
1298	6	2.7	223	2	Q9N9R2	Q9N9R2 leishmania	1371	6	2.7	231	2	Q05484	Q05484 mantoniella
1299	6	2.7	223	2	Q950I5	Q950I5 amnospermop	1372	6	2.7	231	2	Q40351	Q40351 mantoniella
1300	6	2.7	223	2	Q94J89	Q94J89 oryza sativ	1373	6	2.7	231	2	AAB06573	AAB06573 magnapor
1301	6	2.7	223	2	Q72SP3	Q72SP3 leptospira	1374	6	2.7	232	2	Q8TPY1	Q8TPY1 methanosa
1302	6	2.7	223	2	Q8F2W1	Q8F2W1 leptospira	1375	6	2.7	232	2	Q6BNR3	Q6BNR3 debaryomyce
1303	6	2.7	223	2	Q921U2	Q921U2 mus musculu	1376	6	2.7	232	2	Q7U9M6	Q7U9M6 synecococc
1304	6	2.7	223	2	Q90UL1	Q90UL1 mus musculu	1377	6	2.7	232	2	Q87FU6	Q87FU6 vibrio para
1305	6	2.7	223	2	AAS69935	AAS69935 leptospir	1378	6	2.7	233	2	Q7MTH4	Q7MTH4 porphyromon
1306	6	2.7	224	2	Q868T8	Q868T8 plasmodium	1379	6	2.7	233	2	Q8C9U2	Q8C9U2 mus musculu
1307	6	2.7	224	2	Q8S0H3	Q8S0H3 oryza sativ	1380	6	2.7	235	2	Q9VXV3	Q9VXV3 drosophila
1308	6	2.7	224	2	Q6NPF49	Q6NPF49 bdellovibri	1381	6	2.7	235	2	Q7F4G5	Q7F4G5 oryza sativ
1309	6	2.7	224	2	Q7NCD6	Q7NCD6 gloebacter	1382	6	2.7	235	2	Q9LRF3	Q9LRF3 oryza sativ
1310	6	2.7	224	2	CAE78949	CAE78949 bdellovib	1383	6	2.7	235	2	Q07197	Q07197 mycobacteri
1311	6	2.7	225	1	TLV1_ARATH	TLV1_ARATH arabidopsi	1384	6	2.7	235	2	Q7TY32	Q7TY32 mycobacteri
1312	6	2.7	225	2	Q950I7	Q950I7 amnospermop	1385	6	2.7	235	2	Q82885	Q82885 salmonella
1313	6	2.7	225	2	Q950J5	Q950J5 amnospermop	1386	6	2.7	235	2	Q82QP8	Q82QP8 bacterioph
1314	6	2.7	225	2	Q6HFD0	Q6HFD0 bacillus th	1387	6	2.7	236	1	VEAD_BP22	VEAD_BP22 pyrobaculum
1315	6	2.7	225	2	Q72D81	Q72D81 desulfovibr	1388	6	2.7	236	2	Q82XH8	Q82XH8 pyrobaculum
1316	6	2.7	225	2	Q733F4	Q733F4 bacillus ce	1389	6	2.7	236	2	Q6J832	Q6J832 oryza sativ
1317	6	2.7	225	2	Q81V26	Q81V26 bacillus an	1390	6	2.7	236	2	Q75K82	Q75K82 oryza sativ
1318	6	2.7	225	2	Q8Y170	Q8Y170 raistonia s	1391	6	2.7	236	2	Q8ERS3	Q8ERS3 oceanobacil
1319	6	2.7	225	2	AAM13197	AAM13197 arabidops	1392	6	2.7	236	2	AAT07584	AAT07584 oryza sat
1320	6	2.7	225	2	AAP13382	AAP13382 arabidops	1393	6	2.7	236	2	AAT10384	AAT10384 oryza sat
1321	6	2.7	225	2	AAS42609	AAS42609 bacillus	1394	6	2.7	237	1	Y090_HAEIN	Y090_HAEIN haemophilus
1322	6	2.7	225	2	AAS95528	AAS95528 desulfovi	1395	6	2.7	237	2	Q9SBU2	Q9SBU2 cichorium i
1323	6	2.7	225	2	AAT32843	AAT32843 bacillus	1396	6	2.7	237	2	Q9F0X5	Q9F0X5 pseudomonas
1324	6	2.7	226	2	Q950J2	Q950J2 amnospermop	1397	6	2.7	237	2	Q72IH8	Q72IH8 thermus the
1325	6	2.7	226	2	Q950K0	Q950K0 amnospermop	1398	6	2.7	237	2	Q74IA3	Q74IA3 lactobacill
1326	6	2.7	226	2	Q7MQ69	Q7MQ69 vibrio vuln	1399	6	2.7	237	2	Q8D0N1	Q8D0N1 versinia pe
1327	6	2.7	226	2	Q82NR1	Q82NR1 streptomyce	1400	6	2.7	237	2	Q93RV7	Q93RV7 streptomyce
1328	6	2.7	227	1	PYRH_ABRPE	PYRH_ABRPE aeropyrum p	1401	6	2.7	237	2	AAS09435	AAS09435 lactobacac
1329	6	2.7	227	2	Q81EW0	Q81EW0 trypanosoma	1402	6	2.7	237	2	AAS81496	AAS81496 thermus t
1330	6	2.7	227	2	Q7V6P6	Q7V6P6 chrysiptera	1403	6	2.7	238	2	Q9SCP1	Q9SCP1 arabidopsi
1331	6	2.7	227	2	Q7YDQ2	Q7YDQ2 pomacentrus	1404	6	2.7	238	2	Q9FPD9	Q9FPD9 corynebacte
1332	6	2.7	227	2	Q7YDX0	Q7YDX0 chromis ret	1405	6	2.7	238	2	Q9KEL6	Q9KEL6 bacillus ha
1333	6	2.7	227	2	Q7YDX1	Q7YDX1 chromis ret	1406	6	2.7	238	2	Q8CBZ4	Q8CBZ4 mus musculu
1334	6	2.7	227	2	Q7YXP4	Q7YXP4 strongylura	1407	6	2.7	238	2	Q8CBZ4	Q8CBZ4 mus musculu
1335	6	2.7	227	2	Q9T7U3	Q9T7U3 anechura bi	1408	6	2.7	239	1	VV_NDVU2	VV_NDVU2 newcastle d
1336	6	2.7	227	2	Q9TBL3	Q9TBL3 chordelais	1409	6	2.7	239	2	Q7QGS0	Q7QGS0 anopheles g
1337	6	2.7	227	2	Q6Z8Q7	Q6Z8Q7 oryza sativ	1410	6	2.7	239	2	Q6HIV2	Q6HIV2 thermus the
1338	6	2.7	227	2	Q940M1	Q940M1 arabidopsi	1411	6	2.7	239	2	Q746P8	Q746P8 thermus the
1339	6	2.7	227	2	Q8ZDW1	Q8ZDW1 versinia pe	1412	6	2.7	239	2	Q8XRM6	Q8XRM6 raistonia s
1340	6	2.7	227	2	BAD10043	BAD10043 oryza sat	1413	6	2.7	239	2	Q8XVC4	Q8XVC4 raistonia s
1341	6	2.7	227	2	AAS62431	AAS62431 versinia	1414	6	2.7	239	2	Q8N2V9	Q8N2V9 homo sapien
1342	6	2.7	228	1	MTGA_CHRVO	MTGA_CHRVO chromobacte	1415	6	2.7	240	2	Q8N2V9	Q8N2V9 homo sapien
1343	6	2.7	228	2	Q94N53	Q94N53 amnospermop	1416	6	2.7	240	2	Q7PEY3	Q7PEY3 anopheles g
1344	6	2.7	228	2	Q950I4	Q950I4 amnospermop	1417	6	2.7	240	2	P73822	P73822 synecocyst
1345	6	2.7	228	2	Q950I6	Q950I6 amnospermop	1418	6	2.7	240	2	Q8FM52	Q8FM52 corynebacte

1419	6	2.7	240	2	Q8NLI7	Q8nli7 corynebacte
1420	6	2.7	240	2	Q82D63	Q82d63 listeria in
1421	6	2.7	240	2	Q8Y8E6	Q8y8e6 listeria mo
1422	6	2.7	240	2	Q721K8	Q721k8 listeria mo
1423	6	2.7	240	2	CAF20982	CAF20982 corynebac
1424	6	2.7	240	2	AAT03756	AAT03756 listeria
1425	6	2.7	241	2	Q7PWV0	Q7pwv0 anopheles g
1426	6	2.7	241	2	Q7WYU3	Q7wyu3 drosophila
1427	6	2.7	242	1	COMB_SYNXP	Q7u7h6 synecococc
1428	6	2.7	242	1	DAB2_RHIME	Q69783 rhizobium m
1429	6	2.7	242	1	RL1_STRSF	Q7976 streptomyc
1430	6	2.7	242	2	Q7KV06	Q7kv06 drosophila
1431	6	2.7	242	2	Q6TW57	Q6yw57 oryza sativ
1432	6	2.7	242	2	Q8HYS7	Q8hys7 pseudomonas
1433	6	2.7	242	2	Q8XPI6	Q8xpi6 ralstonia s
1434	6	2.7	242	2	Q6O6F2	Q6g6f2 brachydanio
1435	6	2.7	242	2	BAD05832	BAD05832 oryza sat
1436	6	2.7	242	2	AAS66638	AAS66638 brachydan
1437	6	2.7	243	1	AMP_RAT	P24338 rattus norv
1438	6	2.7	243	2	Q88C79	Q88c79 pseudomonas
1439	6	2.7	243	2	Q64608	Q64608 rattus norv
1440	6	2.7	243	2	RS2_BUCAP	Q8k9t0 buchnera ap
1441	6	2.7	244	2	Q75E0	Q75ew0 ashbya gos
1442	6	2.7	244	2	Q875C8	Q875c8 podospira a
1443	6	2.7	244	2	Q76E54	Q76e54 homo sapien
1444	6	2.7	244	2	Q73WV2	Q73wv2 mycobacteri
1445	6	2.7	244	2	Q7U7B8	Q7u7b8 synecococc
1446	6	2.7	244	2	Q8ERX4	Q8erx4 oceanobacil
1447	6	2.7	244	2	AAS04875	AAS04875 mycobacte
1448	6	2.7	244	2	BAD12560	BAD12560 homo sapi
1449	6	2.7	244	2	AAS05334	AAS05334 ashbya go
1450	6	2.7	245	1	YH6C_SCHPO	Q8t8q0 drosophila
1451	6	2.7	246	2	Q78RQ0	Q7f241 oryza sativ
1452	6	2.7	246	2	Q7F241	Q8ln58 oryza sativ
1453	6	2.7	246	2	Q8LN58	Q6neb0 parachlamyd
1454	6	2.7	246	2	Q6NEB0	Q6n531 rhodopseudo
1455	6	2.7	246	2	Q6N531	Q820b6 coxiella bu
1456	6	2.7	246	2	Q820B6	AAL68388 drosophil
1457	6	2.7	246	2	AAL68388	CAE28593 rhodopneu
1458	6	2.7	246	2	CAE28593	CAF23089 parachlam
1459	6	2.7	246	2	CAF23089	Q6pew4 homo sapien
1460	6	2.7	247	2	Q6PEW4	Q8rl61 pseudomonas
1461	6	2.7	247	2	Q8RL61	Q68216 neisseria m
1462	6	2.7	247	2	Q68216	Q8pne4 xanthomonas
1463	6	2.7	247	2	Q8PNE4	Q8xew4 ralstonia s
1464	6	2.7	247	2	Q8XEW4	CAF57838 homo sapi
1465	6	2.7	247	2	AAH57838	P41932 caenorhabdi
1466	6	2.7	248	1	1433_CABEL	P55461 rhizobium s
1467	6	2.7	248	1	Y4GE_RHISN	Q6zsn9 homo sapien
1468	6	2.7	248	2	Q6ZSN9	Q8gpn1 myroides od
1469	6	2.7	248	2	Q8GPN1	Q72ha9 thermus the
1470	6	2.7	248	2	Q72HA9	Q721j1 thermus the
1471	6	2.7	248	2	Q721J1	Q7v3e2 prochloroco
1472	6	2.7	248	2	Q7V3E2	BAC86909 homo sapi
1473	6	2.7	248	2	BAC86909	AAS81483 thermus t
1474	6	2.7	248	2	AAS81483	AAS81928 thermus t
1475	6	2.7	248	2	AAS81928	Q54758 synecococc
1476	6	2.7	249	2	Q54758	Q7c3l0 brachydanio
1477	6	2.7	249	2	Q7C3L0	Q6dd86 homo sapien
1478	6	2.7	250	2	Q6DD86	Q959a7 galaxias an
1479	6	2.7	250	2	Q959A7	Q9rd49 streptomyc
1480	6	2.7	250	2	Q9RD49	Q98nv1 rhizobium l
1481	6	2.7	250	2	Q98NV1	Q9A525 caulobacter
1482	6	2.7	250	2	Q9A525	Q7m5s9 porcine ade
1483	6	2.7	250	2	Q7M5S9	O05410 bacillus au
1484	6	2.7	251	1	YRPE_BACSU	Q9sfc6 arabidopsis
1485	6	2.7	251	2	Q9SFC6	Q7cea4 agrobacteri
1486	6	2.7	251	2	Q7CSA4	Q7dl12 agrobacteri
1487	6	2.7	251	2	Q7DTU72	Q7tut6 prochloroco
1488	6	2.7	251	2	Q7TUT72	Q8lw90 bacillus an
1489	6	2.7	251	2	Q8LW90	Q9x8e2 streptomyc
1490	6	2.7	251	2	Q9X8E2	Q98sw4 rhizobium l
1491	6	2.7	251	2	Q98SW4	

1492	6	2.7	251	2	Q98HG9	Q98hg9 rhizobium l
1493	6	2.7	251	2	Q93J26	Q93j26 streptomyc
1494	6	2.7	251	2	Q8UAK4	Q8uak4 agrobacteri
1495	6	2.7	251	2	O6LLO5	Q6llq5 photobacter
1496	6	2.7	251	2	O8VC08	Q8vc08 mus musculu
1497	6	2.7	251	2	CAG21773	Cag21773 photobact
1498	6	2.7	251	2	AAT33212	AAT33212 bacillus
1499	6	2.7	252	2	Q30850	Q30850 oryctolagus
1500	6	2.7	252	2	Q7F8T0	Q7f8t0 oryza sativ

ALIGNMENTS

RESULT 1

BPPL_HUMAN						
ID	BPPL_HUMAN	STANDARD;	PRT;	223	AA.	
AC	Q96S56; Q8WW74;					
DT	05-JUL-2004 (Rel. 44, Created)					
DT	05-JUL-2004 (Rel. 44, Last sequence update)					
DE	PBP family protein precursor (UNQ1933/PRO4408)					
DE	Homo sapiens (Human)					
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Zhang W., Li N., Wan T., Cao X.,					
RL	Submitted (MAY-2001) to the ENBL/GenBank/DBJ databases.					
RP	[2]					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,					
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,					
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,					
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,					
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,					
RA	Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,					
RA	Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yamaura D.,					
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,					
RA	Godowski P., Gray A.,					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment."					
RL	Genome Res. 13:2265-2270(2003).					
RP	[3]					
RA	SEQUENCE FROM N.A.					
RC	TISSUES=Lung;					
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,					
RA	Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					
RA	Butterfield V.S.N., Kravinsky M.I., Skalska U., Smalish D.E.,					
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;					
RT	"Generation and initial analysis of more than 15,000 full-length human					
RT	and mouse cDNA sequences."					
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
CC	-!- SURCELLULAR LOCATION: Secreted (Potential).					
CC	-!- SIMILARITY: Belongs to the phosphatidylethanolamine-binding					
CC	protein family.					

DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 FT NON TER 151 151
 SQ SEQUENCE 151 AA; 17038 MW; FCC66D7F1D7E3974 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.093;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 LVMVDPDAPS 101
 Db 67 LVMVDPDAPS 76
 |||||

RESULT 4

ID CAES3888 PRELIMINARY; PRT; 151 AA.
 AC CAES3888;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE Putative PBP protein (Fragment).
 GN HD3A.
 OS *Triticum aestivum* (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chinese Spring; TISSUE=Spike at heading stage;
 RA Ciaffi M., Tanzarella O.A., Porceddu E., Paolacci A.R., d'Aloisio E.;
 RT "Identification and characterization of gene sequences expressed in
 wheat spikelets at the heading stage";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ577367; CAES3888.1; --
 FT NON TER 151 151
 SQ SEQUENCE 151 AA; 17038 MW; FCC66D7F1D7E3974 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.093;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 LVMVDPDAPS 101
 Db 67 LVMVDPDAPS 76
 |||||

RESULT 5

ID Q75QX2 PRELIMINARY; PRT; 173 AA.
 AC Q75QX2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Flowering locus T.
 GN Name=PnFT3a;
 OS *Populus nigra* (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nishiguchi M., Nanjo T., Kotoda N.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB161107; BAD08336.1; --
 DR InterPro; IPR001858; PBP.
 DR InterPro; IPR008914; PBP.
 DR Pfam; PF01161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 SQ SEQUENCE 173 AA; 19521 MW; 291C4FC5A50754B2 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 173;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 LVMVDPDAPS 101
 Db 66 LVMVDPDAPS 75
 |||||

RESULT 6

ID Q6R3R0 PRELIMINARY; PRT; 174 AA.
 AC Q6R3R0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Flowering locus T-like protein FT1.
 OS *Populus deltoides* (Poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3696;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuceer C., Land S.B. Jr., Luth D.S.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY515152; AAS00056.1; --
 DR InterPro; IPR001858; PBP.
 DR InterPro; IPR008914; PBP.
 DR Pfam; PF01161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 SQ SEQUENCE 174 AA; 19655 MW; B70F1787152584D7 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 LVMVDPDAPS 101
 Db 66 LVMVDPDAPS 75
 |||||

RESULT 7

ID Q75QW8 PRELIMINARY; PRT; 174 AA.
 AC Q75QW8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Flowering locus T like protein.
 GN Name=MFT;
 OS *Malus domestica* (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 OX NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kotoda N., Igasaki T., Abe K.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB161112; BAD08340.1; --
 DR InterPro; IPR001858; PBP.
 DR InterPro; IPR008914; PBP.
 DR Pfam; PF01161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 SQ SEQUENCE 174 AA; 19532 MW; 3714BF80E0E290FA CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
 |||||
 Db 66 LVMVDPDAPS 75

RESULT 8
 Q76BW3 PRELIMINARY; PRT; 174 AA.
 AC Q76BW3
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DE Flowering locus T.
 GN Name=PnFT2c;
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nanjo T., Nishiguchi M., Kotoda N.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB110613; BAD02372.1; -;
 DR InterPro; IPR001858; PBP.
 DR Pfam; PF01161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 SQ SEQUENCE 174 AA; 19655 MW; B70F1787152584D7 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
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 Db 66 LVMVDPDAPS 75

RESULT 9
 Q76BW4 PRELIMINARY; PRT; 174 AA.
 AC Q76BW4
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DE Flowering locus T.
 GN Name=PnFT2b;
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nanjo T., Nishiguchi M., Kotoda N.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB110612; BAD02371.1; -;
 DR InterPro; IPR001858; PBP.
 DR Pfam; PF01161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 SQ SEQUENCE 174 AA; 19590 MW; 929827E93409E005 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
 |||||

Db 66 LVMVDPDAPS 75

RESULT 10
 Q76CA4 PRELIMINARY; PRT; 174 AA.
 AC Q76CA4
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DE Flowering locus T.
 GN Name=PnFT2a;
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nanjo T., Nishiguchi M., Kotoda N.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB110009; BAD01576.1; -;
 DR InterPro; IPR001858; PBP.
 DR Pfam; PF01161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 SQ SEQUENCE 174 AA; 19563 MW; 9289C61925E81005 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
 |||||
 Db 66 LVMVDPDAPS 75

RESULT 11
 Q76CC3 PRELIMINARY; PRT; 174 AA.
 AC Q76CC3
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DE Flowering locus T.
 GN Name=PnFT1b; Synonyms=PnFT4a;
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nanjo T., Nishiguchi M., Kotoda N.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nishiguchi M., Nanjo T., Kotoda N.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB109804; BAD01561.1; -;
 DR EMBL; AB161108; BAD08337.1; -;
 DR InterPro; IPR001858; PBP.
 DR Pfam; PF01161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 SQ SEQUENCE 174 AA; 19629 MW; A34A03C2152584D7 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
 DB |||||||
 66 LVMVDPDAPS 75

RESULT 12
 Q76EQ5 PRELIMINARY; PRT; 174 AA.
 AC Q76EQ5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Flowering locus T.
 GN Name=PnFT1a; Synonyms=PnFT4b;
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nishiguchi M., Furtamura N., Nanjo T., Kotoda N.;
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RL Submited (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB106111; BAD01612.1; -;
 DR EMBL; AB161109; BAD08338.1; -;
 DR InterPro; IPR001858; PBP.
 DR InterPro; IPR008914; PBP.
 DR Pfam; PF01161; PBP; 1.
 DR ProDom; PD004330; PBP; 1.
 DR PROSITE; PS01220; PBP; 1.
 SQ SEQUENCE 174 AA; 19661 MW; BEE0B4C21531C087 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
 DB |||||||
 66 LVMVDPDAPS 75

RESULT 13
 BAD01561 PRELIMINARY; PRT; 174 AA.
 AC BAD01561;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Flowering locus T.
 GN PnFT1b.
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nanjo T., Nishiguchi M., Kotoda N.;
 RT "Populus nigra mRNA for flowering locus T (PnFT1b), complete cds.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB109804; BAD01561.1; -;
 SQ SEQUENCE 174 AA; 19629 MW; A34A03C2152584D7 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
 DB |||||||

Db 66 LVMVDPDAPS 75

RESULT 14
 BAD01576 PRELIMINARY; PRT; 174 AA.
 AC BAD01576;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Flowering locus T.
 GN PnFT2a.
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nanjo T., Nishiguchi M., Kotoda N.;
 RT "Populus nigra mRNA for flowering locus T (PnFT2a), complete cds.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB110009; BAD01576.1; -;
 SQ SEQUENCE 174 AA; 19563 MW; 9289C61925E81005 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
 DB |||||||
 66 LVMVDPDAPS 75

RESULT 15
 BAD01612 PRELIMINARY; PRT; 174 AA.
 AC BAD01612;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Flowering locus T.
 GN PnFT1a.
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igasaki T., Nishiguchi M., Furtamura N., Nanjo T., Kotoda N.;
 RT "Populus nigra flowering locus T (FT) gene complete cds.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB106111; BAD01612.1; -;
 SQ SEQUENCE 174 AA; 19661 MW; BEE0B4C21531C087 CRC64;

Query Match 4.5%; Score 10; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDPDAPS 101
 DB |||||||
 66 LVMVDPDAPS 75

Search completed: January 31, 2005, 15:14:16
 Job time : 133.secs

87	223	100.0	223	14	US-10-223-090-306	Sequence 306, App	160	85	38.1	205	16	US-10-403-142-116	Sequence 116, App
88	223	100.0	223	14	US-10-219-070-232	Sequence 232, App	161	85	38.1	209	16	US-10-403-142-112	Sequence 112, App
89	223	100.0	223	14	US-10-219-472-232	Sequence 232, App	162	72	32.3	86	10	US-09-895-298-112	Sequence 112, App
90	223	100.0	223	14	US-10-219-527-232	Sequence 232, App	163	72	32.3	86	10	US-09-895-298-224	Sequence 224, App
91	223	100.0	223	14	US-10-227-877-232	Sequence 232, App	164	72	32.3	86	10	US-10-885-039-112	Sequence 112, App
92	223	100.0	223	14	US-10-223-087-306	Sequence 306, App	165	72	32.3	86	10	US-10-885-039-224	Sequence 224, App
93	223	100.0	223	14	US-10-223-083-306	Sequence 306, App	166	59	26.5	84	17	US-10-425-115-312177	Sequence 312177, App
94	223	100.0	223	14	US-10-216-166-232	Sequence 232, App	167	23	10.3	23	10	US-09-895-298-220	Sequence 220, App
95	223	100.0	223	14	US-10-218-612-232	Sequence 232, App	168	22	10.3	23	10	US-09-895-298-220	Sequence 220, App
96	223	100.0	223	14	US-10-223-089-306	Sequence 306, App	169	22	9.9	24	10	US-09-895-298-219	Sequence 219, App
97	223	100.0	223	14	US-10-035-977-61	Sequence 61, Appl	170	22	9.9	24	10	US-10-885-039-219	Sequence 219, App
98	223	100.0	223	14	US-10-216-163-232	Sequence 232, App	171	20	9.0	20	10	US-09-895-298-221	Sequence 221, App
99	223	100.0	223	14	US-10-223-081-306	Sequence 306, App	172	20	9.0	20	10	US-10-885-039-221	Sequence 221, App
100	223	100.0	223	14	US-10-218-765-232	Sequence 232, App	173	17	7.6	17	10	US-09-895-298-222	Sequence 222, App
101	223	100.0	223	14	US-10-219-063-232	Sequence 232, App	174	17	7.6	17	10	US-10-885-039-222	Sequence 222, App
102	223	100.0	223	14	US-10-219-066-232	Sequence 232, App	175	14	6.3	21	10	US-09-895-298-217	Sequence 217, App
103	223	100.0	223	14	US-10-219-067-232	Sequence 232, App	176	14	6.3	21	10	US-10-885-039-217	Sequence 217, App
104	223	100.0	223	14	US-10-219-068-232	Sequence 232, App	177	14	6.3	83	10	US-09-895-298-215	Sequence 215, App
105	223	100.0	223	14	US-10-219-069-232	Sequence 232, App	178	14	6.3	83	10	US-09-895-298-215	Sequence 215, App
106	223	100.0	223	14	US-10-219-073-232	Sequence 232, App	179	10	4.5	87	17	US-10-425-115-211755	Sequence 211755, App
107	223	100.0	223	14	US-10-219-475-232	Sequence 232, App	180	10	4.5	89	16	US-10-655-799-27	Sequence 27, Appl
108	223	100.0	223	14	US-10-219-480-232	Sequence 232, App	181	10	4.5	140	17	US-10-425-115-261245	Sequence 261245, App
109	223	100.0	223	14	US-10-219-483-232	Sequence 232, App	182	10	4.5	168	16	US-10-767-701-51924	Sequence 51924, A
110	223	100.0	223	14	US-10-219-525-232	Sequence 232, App	183	10	4.5	177	15	US-10-424-599-274975	Sequence 274975, App
111	223	100.0	223	14	US-10-219-526-232	Sequence 232, App	184	10	4.5	177	16	US-10-655-799-26	Sequence 26, Appl
112	223	100.0	223	14	US-10-219-530-232	Sequence 232, App	185	10	4.5	177	16	US-10-425-115-243651	Sequence 243651, App
113	223	100.0	223	14	US-10-219-531-232	Sequence 232, App	186	10	4.5	178	16	US-10-437-963-172754	Sequence 172754, App
114	223	100.0	223	14	US-10-219-532-232	Sequence 232, App	187	10	4.5	179	15	US-10-425-114-56802	Sequence 56802, A
115	223	100.0	223	14	US-10-219-533-232	Sequence 232, App	188	10	4.5	179	15	US-10-432-531-2	Sequence 2, Appl
116	223	100.0	223	14	US-10-230-437-232	Sequence 232, App	189	10	4.5	197	16	US-10-437-963-168356	Sequence 168356, A
117	223	100.0	223	14	US-10-232-228-232	Sequence 232, App	190	10	4.5	213	15	US-10-425-114-73066	Sequence 73066, A
118	223	100.0	223	14	US-10-223-082-306	Sequence 306, App	191	10	4.5	232	16	US-10-437-963-113293	Sequence 113293, App
119	223	100.0	223	14	US-10-305-654-306	Sequence 306, App	192	10	4.5	276	17	US-10-491-733-44	Sequence 44, Appl
120	223	100.0	223	15	US-10-232-226-232	Sequence 232, App	193	10	4.5	485	16	US-10-437-963-148986	Sequence 148986, App
121	223	100.0	223	15	US-10-230-130-232	Sequence 232, App	194	9	4.0	185	16	US-10-437-963-116665	Sequence 116665, App
122	223	100.0	223	15	US-10-081-086-306	Sequence 306, App	195	8	3.6	59	16	US-10-311-174A-85	Sequence 85, Appl
123	223	100.0	223	15	US-10-219-535-232	Sequence 232, App	196	8	3.6	69	9	US-09-764-853-536	Sequence 536, App
124	223	100.0	223	15	US-10-232-230-232	Sequence 232, App	197	8	3.6	141	9	US-09-764-891-3399	Sequence 3399, App
125	223	100.0	223	15	US-10-119-480-232	Sequence 232, App	198	8	3.6	141	10	US-09-791-572-282	Sequence 282, App
126	223	100.0	223	15	US-10-219-477-232	Sequence 232, App	199	8	3.6	141	14	US-10-091-438-175	Sequence 175, App
127	223	100.0	223	17	US-10-884-091-61	Sequence 61, Appl	200	8	3.6	141	14	US-10-264-049-2668	Sequence 2668, App
128	224	96.0	227	16	US-10-403-142-128	Sequence 128, App	201	8	3.6	147	15	US-10-437-963-138695	Sequence 138695, App
129	210	94.2	227	11	US-09-978-360A-540	Sequence 540, App	202	8	3.6	169	9	US-09-815-242-10795	Sequence 10795, A
130	210	94.2	227	15	US-10-403-676-76	Sequence 76, Appl	203	8	3.6	316	15	US-10-282-122A-57056	Sequence 57056, A
131	210	94.2	227	16	US-10-403-142-108	Sequence 108, App	204	8	3.6	316	15	US-10-282-122A-60415	Sequence 60415, A
132	210	94.2	227	16	US-10-403-142-130	Sequence 130, App	205	8	3.6	328	15	US-10-282-122A-74524	Sequence 74524, A
133	210	94.2	235	15	US-10-403-676-62	Sequence 62, Appl	206	8	3.6	344	15	US-10-282-122A-67763	Sequence 67763, A
134	198	88.8	206	15	US-10-403-676-66	Sequence 66, Appl	207	8	3.6	439	14	US-10-369-493-18616	Sequence 18616, A
135	189	84.8	227	16	US-10-403-142-118	Sequence 118, App	208	8	3.6	521	14	US-10-369-493-17839	Sequence 17839, A
136	188	84.3	205	15	US-10-403-676-78	Sequence 78, Appl	209	8	3.6	693	15	US-10-108-260A-3849	Sequence 3849, App
137	188	84.3	209	16	US-10-403-142-114	Sequence 114, App	210	8	3.6	14	9	US-09-791-378-135	Sequence 135, App
138	188	84.3	211	15	US-10-403-676-70	Sequence 70, Appl	211	7	3.1	14	9	US-09-791-378-587	Sequence 587, App
139	175	78.9	182	15	US-10-403-676-72	Sequence 72, Appl	212	7	3.1	14	10	US-09-988-493-277	Sequence 277, App
140	175	78.5	227	16	US-10-403-142-120	Sequence 120, App	213	7	3.1	14	10	US-09-988-493-277	Sequence 277, App
141	159	71.3	227	16	US-10-403-142-126	Sequence 126, App	214	7	3.1	14	11	US-09-791-377-135	Sequence 135, App
142	124	55.6	182	14	US-10-291-265-717	Sequence 717, App	215	7	3.1	14	11	US-09-791-377-587	Sequence 587, App
143	124	55.6	206	15	US-10-403-676-64	Sequence 64, Appl	216	7	3.1	14	14	US-10-014-340-528	Sequence 528, App
144	124	55.6	223	14	US-10-291-265-245	Sequence 245, App	217	7	3.1	14	15	US-10-449-829A-32	Sequence 32, Appl
145	124	55.6	227	10	US-09-895-298-107	Sequence 107, App	218	7	3.1	14	15	US-10-601-837-154	Sequence 154, App
146	124	55.6	227	10	US-09-879-401-3	Sequence 3, Appl	219	7	3.1	22	10	US-09-766-511B-4	Sequence 4, Appl
147	124	55.6	227	13	US-10-003-152-2	Sequence 2, Appl	220	7	3.1	22	10	US-10-042-431-28	Sequence 28, Appl
148	124	55.6	227	14	US-10-002-050-2	Sequence 2, Appl	221	7	3.1	22	13	US-10-425-115-285808	Sequence 168808, App
149	124	55.6	227	14	US-10-002-304-2	Sequence 58, Appl	222	7	3.1	34	16	US-10-437-963-168808	Sequence 285839, A
150	124	55.6	227	15	US-10-403-676-58	Sequence 124, App	223	7	3.1	48	17	US-10-425-115-285839	Sequence 29003, A
151	124	55.6	227	16	US-10-403-142-124	Sequence 107, App	224	7	3.1	55	14	US-10-029-386-29003	Sequence 135738, App
152	124	55.6	235	17	US-10-885-039-107	Sequence 60, Appl	225	7	3.1	75	16	US-10-437-963-135738	Sequence 135403, App
153	124	55.6	235	15	US-10-403-676-60	Sequence 218, App	226	7	3.1	89	11	US-09-864-408A-4420	Sequence 4420, App
154	120	53.8	149	10	US-09-895-298-218	Sequence 218, App	227	7	3.1	89	11	US-10-437-963-185403	Sequence 185403, App
155	120	53.8	149	17	US-10-885-039-218	Sequence 218, App	228	7	3.1	99	15	US-10-767-701-31925	Sequence 31925, A
156	109	48.9	227	16	US-10-403-142-122	Sequence 122, App	229	7	3.1	106	17	US-10-425-115-241781	Sequence 241781, App
157	102	45.7	182	15	US-10-403-676-74	Sequence 74, Appl	230	7	3.1	112	16	US-10-425-115-241781	Sequence 135491, App
158	102	45.7	211	15	US-10-403-676-68	Sequence 68, Appl	231	7	3.1	112	16	US-10-437-963-135491	Sequence 536, App
159	96	43.0	209	16	US-10-403-142-110	Sequence 110, App	232	7	3.1	114	11	US-09-864-408A-536	

233	7	3.1	124	17	US-10-425-115-216896	Sequence 216896,	306	7	3.1	250	10	US-09-847-513A-43	Sequence 43, Appl
234	7	3.1	125	16	US-10-437-963-201902	Sequence 201902,	307	7	3.1	250	10	US-09-847-513A-45	Sequence 45, Appl
235	7	3.1	126	16	US-10-767-701-52363	Sequence 52363, A	308	7	3.1	250	10	US-09-847-513A-47	Sequence 47, Appl
236	7	3.1	128	16	US-10-437-963-145872	Sequence 145872,	309	7	3.1	252	14	US-10-304-928-20	Sequence 20, Appl
237	7	3.1	129	14	US-10-168-048A-11	Sequence 11, Appl	310	7	3.1	257	17	US-10-425-115-269207	Sequence 269207,
238	7	3.1	129	14	US-10-094-479-2798	Sequence 2798, Ap	311	7	3.1	263	15	US-10-425-114-50588	Sequence 50588, A
239	7	3.1	135	14	US-10-101-464A-618	Sequence 618, App	312	7	3.1	263	15	US-10-425-114-60148	Sequence 60148, A
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241	7	3.1	140	16	US-10-408-765A-260	Sequence 260, App	314	7	3.1	265	15	US-10-425-114-48471	Sequence 48471, A
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297	7	3.1	250	10	US-09-847-513A-39	Sequence 39, Appl	370	7	3.1	553	16	US-10-653-517-5	Sequence 5, Appli
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412	7	3.1	669	16	US-10-653-497-25	Sequence 25, Appli	485	6	2.7	65	11	US-09-864-408A-5100	Sequence 5100, App
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543	6	2.7	86	17	US-10-424-599-264442	Sequence 264442,	616	6	2.7	106	9	US-09-845-849-8	Sequence 8, Appli
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ALIGNMENTS

RESULT 1

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; Sequence 61, Application US/09931836
; Publication No. US2003002749A1
; GENERAL INFORMATION:
; APPLICANT: Destoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C1
; CURRENT APPLICATION NUMBER: US/09/931,836
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
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; PRIOR FILING DATE: 1999-01-22
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; PRIOR FILING DATE: 1999-03-23
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; PRIOR FILING DATE: 2001-06-01
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-931-836-61

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Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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; GENERAL INFORMATION:
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C5
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; PRIOR FILING DATE: 1998-12-23
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; PRIOR FILING DATE: 1999-01-12
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; PRIOR FILING DATE: 1999-01-22
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; PRIOR FILING DATE: 2000-12-20
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; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-342-61

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Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C8
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; CURRENT FILING DATE: 2001-12-26
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PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 61
LENGTH: 223
TYPE: PRT
ORGANISM: Homo Sapien
US-10-035-855-61

Query Match 100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVPYFPELGNIGCKV 60

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QY 121 ADLKKGIQOGELSAYQAPSPAHSGFHRYPFFVYLBQGVISLLPKENKTRGSMWMDRF 180
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QY 181 LNRPHLGEPEASTQPMTONYQDSPTLOAPGRASEPKHKTROR 223
Db 181 LNRPHLGEPEASTQPMTONYQDSPTLOAPGRASEPKHKTROR 223

RESULT 5
US-10-227-884-232
Sequence 232, Application US/10227884
Publication No. US20030027988A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC79
CURRENT APPLICATION NUMBER: US/10/227,884
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1999-01-12
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PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19

;; PRIOR APPLICATION NUMBER: 60/125775
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;; PRIOR FILING DATE: 1999-03-29
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;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/130232
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/131022
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;; PRIOR APPLICATION NUMBER: 60/131291
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;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/140723
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;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
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;; PRIOR FILING DATE: 1999-07-28
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;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGMTWRLVTAALLGLMMVVTGDEBNSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60
Db 1 MGMTWRLVTAALLGLMMVVTGDEBNSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60

Qy 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGTATYILVMVDDPDAPSRAEPRQFRWHLVTDIKG 120
Db 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGTATYILVMVDDPDAPSRAEPRQFRWHLVTDIKG 120

Qy 121 ADLKKGKIQGQSLSAQAPSPAHSGFHYQFVVLQEGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKKGKIQGQSLSAQAPSPAHSGFHYQFVVLQEGKVISLLPKENKTRGSKWMDRF 180

Qy 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPGRGRASPEPKHKTOR 223
Db 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPGRGRASPEPKHKTOR 223

RESULT 6
US-10-036-214-61
; Sequence 61, Application US/10036214
; Publication No. US20030032061A1

;; GENERAL INFORMATION:
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P3030R1C11
;; CURRENT APPLICATION NUMBER: US/10/036.214
;; CURRENT FILING DATE: 2001-12-26
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/112514
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113300
;; PRIOR FILING DATE: 1998-12-22
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;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/114140
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115552
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/116843
;; PRIOR FILING DATE: 1999-01-22
;; PRIOR APPLICATION NUMBER: 60/125774
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/125778
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;; PRIOR FILING DATE: 1999-03-24
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;; PRIOR APPLICATION NUMBER: 60/132379
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;; PRIOR APPLICATION NUMBER: 60/135750
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/138166
;; PRIOR FILING DATE: 1999-06-08
;; PRIOR APPLICATION NUMBER: 60/144791
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;; PRIOR APPLICATION NUMBER: 60/146970
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;; PRIOR APPLICATION NUMBER: 60/162506
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: 09/311832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 09/380142

;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/644848
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 09/747259
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;; PRIOR APPLICATION NUMBER: 09/816744
;; PRIOR FILING DATE: 2001-03-22
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;; PRIOR APPLICATION NUMBER: 09/854280
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: 09/874503
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: 09/869599
;; PRIOR FILING DATE: 2001-06-29
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;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/23328
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;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
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;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
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;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 80
;; SEQ ID NO 61
;; LENGTH: 223
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-036-214-61

Query Match 100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGTWRLVTAALLGLMNVVTVGDEENSPCAHEALLDEDTLFCQGLEVFYPBELGNIGCKV 60
DB 1 MGTWRLVTAALLGLMNVVTVGDEENSPCAHEALLDEDTLFCQGLEVFYPBELGNIGCKV 60
QY 61 VPCNNYRKITSWMEPIVKFPGVDGATYILVMVDPDAPSAEPRQFRWHLVTDIKG 120
DB 61 VPCNNYRKITSWMEPIVKFPGVDGATYILVMVDPDAPSAEPRQFRWHLVTDIKG 120
QY 121 ADLKKGKIQQBELSAQAPSPAHSGFHRYPFVYLQEGKVLSLLPKENKTRGSWMDRF 180
DB 121 ADLKKGKIQQBELSAQAPSPAHSGFHRYPFVYLQEGKVLSLLPKENKTRGSWMDRF 180
QY 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223

Db 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223
RESULT 7
US-10-035-719-61
;; Sequence 61, Application US/10035719
;; Publication No. US20030036114A1
;; GENERAL INFORMATION:
;; APPLICANT: Desnoyers,Luc
;; APPLICANT: Eaton,Dan L.
;; APPLICANT: Goddard,Audrey
;; APPLICANT: Godowski,Paul J.
;; APPLICANT: Gurney,Austin L.
;; APPLICANT: Pan,James
;; APPLICANT: Stewart,Timothy A.
;; APPLICANT: Watanabe,Colin K.
;; APPLICANT: Wood,William I.
;; APPLICANT: Zhang,Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3030R1C2
;; CURRENT APPLICATION NUMBER: US/10/035,719
;; CURRENT FILING DATE: 2001-12-26
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 80
;; SEQ ID NO 61
;; LENGTH: 223
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-035-719-61

Query Match 100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MGTWRLVTAALLGLMVMVVDGDENSPCAHEALLDDETLFCQGLEVFYFELGNIGCKV 60
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DB 1 MGTWRLVTAALLGLMVMVVDGDENSPCAHEALLDDETLFCQGLEVFYFELGNIGCKV 60
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OY 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGYATYILVMVDPDAPSAEPRQRFWRHLVTDIKG 120

Db 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGYATYILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
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OY 121 ADLKKGKIQQGELSAYQAPSPAHSGFHRHYOFFVYVLOQSGKVISLIPKKNKTRGSKWMDRF 180
|||||
Db 121 ADLKKGKIQQGELSAYQAPSPAHSGFHRHYOFFVYVLOQSGKVISLIPKKNKTRGSKWMDRF 180
|||||
OY 181 LNRPHLGEPEASTQFMTQNYQDSPTLQAPGRASEPKHKTRQR 223
|||||
Db 181 LNRPHLGEPEASTQFMTQNYQDSPTLQAPGRASEPKHKTRQR 223
|||||

RESULT 8

US-10-230-163-232
; Sequence 232, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC96
; CURRENT APPLICATION NUMBER: US/10/230.163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2,4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGTWRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPPELGNIGCKV 60
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QY 61 VPDCCNYRQKITSWNEPIVKFPGAVDGTATYLLVMVDDPAPSAEPRQRFWRHMLVTDIKG 120
DB 61 VPDCCNYRQKITSWNEPIVKFPGAVDGTATYLLVMVDDPAPSAEPRQRFWRHMLVTDIKG 120
QY 121 ADLKGKIQGBLSAYQAPSPHAGPHRYQFVYVLOGBKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQGBLSAYQAPSPHAGPHRYQFVYVLOGBKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRPHLGEPEASTQPMYQNSPTLOAPRGASEPKIKTROR 223
DB 181 LNRPHLGEPEASTQPMYQNSPTLOAPRGASEPKIKTROR 223

RESULT 9

US-10-036-160-61
; Sequence 61, Application US/10036160
; Publication No. US20030044842A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C3
; CURRENT APPLICATION NUMBER: US/10/036,160
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 223

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-160-61

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Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGWTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYPYELGNIGCKV 60

QY 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAPRQRFWRHLVTDIKG 120
DB 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAPRQRFWRHLVTDIKG 120

QY 121 ADLKGKIQGELSAYQAPSPAHSGFHRYPQFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQGELSAYQAPSPAHSGFHRYPQFVYLOEGKVISLLPKENKTRGSKWMDRF 180

QY 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223
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RESULT 10
US-10-230-338-232
; Sequence 232, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 232
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-232
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Best Local Similarity 100.0%; Pred. No. 2.4e-210;
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DB 61 VPDNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAPRQRFWRHLVTDIKG 120

QY 121 ADLKGKIQGELSAYQAPSPAHSGFHRYPQFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQGELSAYQAPSPAHSGFHRYPQFVYLOEGKVISLLPKENKTRGSKWMDRF 180

QY 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223
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RESULT 11
US-10-218-631-232
; Sequence 232, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC14
; CURRENT APPLICATION NUMBER: US/10/218,631
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
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; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 232
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-232
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Query Match      100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.4e-210;
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Db 1 MGMTMLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPGLGNIGCKV 60
QY 61 VPDCCNYRQKITSWNEPIVKFPGAVDGTATYILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
Db 61 VPDCCNYRQKITSWNEPIVKFPGAVDGTATYILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
QY 121 ADLKGKIQQLSAYQAPSPPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKMDRF 180
Db 121 ADLKGKIQQLSAYQAPSPPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKMDRF 180
QY 181 LNRFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223
Db 181 LNRFLGPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 12
US-10-035-958-61
; Sequence 61, Application US/10035958
; Publication No. US20030049733A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030RIC7
; CURRENT APPLICATION NUMBER: US/10/035,958
; CURRENT FILING DATE: 2001-12-26
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; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
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; SEQ ID NO 61
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-035-958-61

Query Match      100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2,4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGMTMLRVTAALLGLMMVVTGDEDENSPCAHEALLDDETLFCQGLEVFYPELGNIGCKV 60

QY 61 VPCNNYRKITSWMEPIVKFPGAVDGTATVLMVDPDAPSRAEPQRWRHVLVTDIKG 120
Db 61 VPCNNYRKITSWMEPIVKFPGAVDGTATVLMVDPDAPSRAEPQRWRHVLVTDIKG 120

QY 121 ADLKKGKIQQEELSAQCAPSPPAHSGFHRVQFFVYLQEGKVISLLPKENKTRGSKWQDRF 180
Db 121 ADLKKGKIQQEELSAQCAPSPPAHSGFHRVQFFVYLQEGKVISLLPKENKTRGSKWQDRF 180

QY 181 LNRPHLGEPEASTQFTQNTQYQDSPTLQAPRGRASEPKHKTQR 223
Db 181 LNRPHLGEPEASTQFTQNTQYQDSPTLQAPRGRASEPKHKTQR 223

RESULT 13
US-10-036-150-61
; Sequence 61, Application US/10036150
; Publication No. US20030049734A1
; GENERAL INFORMATION:
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P30301C9
; CURRENT APPLICATION NUMBER: US/10/036,150
; PRIOR FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
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; PRIOR FILING DATE: 1999-01-22
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; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
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; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
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; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
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; PRIOR APPLICATION NUMBER: 09/816744
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; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
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; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
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; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
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; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 61
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-150-61

Query Match 100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPYELGNIGCKV 60
DB 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPYELGNIGCKV 60

QY 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGYILVMVDPDAPSRAPRQRFWRHVLVTDIKG 120
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DB 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 14

US-10-230-414-232
; Sequence 232, Application US/10230414
; Publication No. US20030050448A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 232
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-232

Query Match 100.0%; Score 223; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGWTRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPYELGNIGCKV 60

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DB 121 ADLKGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSKWMDRF 180

QY 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRFLHGEPEASTQFMNTQYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 15

US-10-232-224-232
; Sequence 232, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C111
; CURRENT APPLICATION NUMBER: US/10/232,224
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 232

; LENGTH: 223

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-232-224-232

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Best Local Similarity 100.0%; Pred. No. 2.4e-210;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  MCGTWRLVTAALLGLMMVVTGDEDNSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60

QY      61  VPDCCNNYRQKITSWMEPIVKFPGAVDGYTILVMVDPDAPSRAEPRQRFWRHVLVTDIKG 120
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QY      121  ADLKKGKIQQBELSAYQAPSPPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKWMDRF 180
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Db      121  ADLKKGKIQQBELSAYQAPSPPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKWMDRF 180

QY      181  LNRFHGLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223
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Db      181  LNRFHGLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223
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Search completed: January 31, 2005, 15:17:31
Job time : 92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2005, 15:11:04 ; Search time 22 Seconds
(without alignments)
672.223 Million cell updates/sec

Title: US-10-035-958-61

Perfect score: 223

Sequence: 1 MGWTRLVTAALLGLMMVV.....PTLQAPGRASEPKHKTRQ 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 6

Total number of hits satisfying chosen parameters: 626

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:**

4: /cgn2_6/prodata/1/1aa/6B-COMB.pep:**

5: /cgn2_6/prodata/1/1aa/PCTUS-COMB.pep:**

6: /cgn2_6/prodata/1/1aa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	210	94.2	227	4	US-09-621-976-8
2	210	94.2	227	4	US-09-513-999C-8
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4	8	3.6	116	4	US-09-248-796A-21372
5	8	3.6	137	2	US-08-974-546-3
6	8	3.6	143	4	US-09-621-976-7099
7	8	3.6	190	4	US-09-134-000C-4833
8	7	3.1	15	1	US-08-403-378B-7
9	7	3.1	22	4	US-09-578-063-28
10	7	3.1	110	4	US-09-252-991A-25566
11	7	3.1	115	4	US-09-252-991A-29066
12	7	3.1	135	4	US-10-101-464A-618
13	7	3.1	141	4	US-09-270-767-43926
14	7	3.1	152	1	US-07-644-372-2
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19	7	3.1	172	4	US-09-578-063-74
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21	7	3.1	175	4	US-09-845-849A-2
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23	7	3.1	186	4	US-09-492-308A-8
24	7	3.1	187	1	US-08-403-378B-4
25	7	3.1	187	1	US-08-403-378B-15
26	7	3.1	187	4	US-09-492-308A-7
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28	7	3.1	252	4	US-09-522-714-20	Sequence 20, Appl
29	7	3.1	333	4	US-10-101-464A-561	Sequence 561, App
30	7	3.1	375	1	US-08-027-986-1	Sequence 1, Appl
31	7	3.1	375	1	US-08-027-986-2	Sequence 2, Appl
32	7	3.1	458	4	US-09-252-991A-27645	Sequence 27645, A
33	7	3.1	463	4	US-09-248-796A-25246	Sequence 25246, A
34	7	3.1	495	3	US-08-984-618-5	Sequence 5, Appl
35	7	3.1	540	4	US-09-213-888-7	Sequence 7, Appl
36	7	3.1	540	4	US-09-213-888-10	Sequence 10, Appl
37	7	3.1	540	4	US-09-328-877D-7	Sequence 7, Appl
38	7	3.1	540	4	US-09-328-877D-10	Sequence 10, Appl
39	7	3.1	541	4	US-09-134-000C-5420	Sequence 5420, Ap
40	7	3.1	545	4	US-09-213-888-6	Sequence 6, Appl
41	7	3.1	545	4	US-09-328-877D-6	Sequence 6, Appl
42	7	3.1	553	4	US-09-213-888-5	Sequence 5, Appl
43	7	3.1	553	4	US-09-328-877D-5	Sequence 5, Appl
44	7	3.1	559	4	US-09-213-888-9	Sequence 9, Appl
45	7	3.1	559	4	US-09-328-877D-9	Sequence 9, Appl
46	7	3.1	589	4	US-09-213-888-8	Sequence 8, Appl
47	7	3.1	589	4	US-09-328-877D-8	Sequence 8, Appl
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49	7	3.1	592	4	US-09-328-877D-4	Sequence 4, Appl
50	7	3.1	626	3	US-08-961-083-220	Sequence 220, App
51	7	3.1	626	4	US-09-536-784-220	Sequence 220, App
52	7	3.1	626	4	US-09-213-888-21	Sequence 21, Appl
53	7	3.1	626	4	US-09-328-877D-21	Sequence 21, Appl
54	7	3.1	627	4	US-09-213-888-3	Sequence 3, Appl
55	7	3.1	627	4	US-09-328-877D-3	Sequence 3, Appl
56	7	3.1	664	4	US-09-252-991A-31745	Sequence 31745, A
57	7	3.1	666	4	US-09-213-888-27	Sequence 27, Appl
58	7	3.1	666	4	US-09-328-877D-27	Sequence 27, Appl
59	7	3.1	669	4	US-09-213-888-25	Sequence 25, Appl
60	7	3.1	669	4	US-09-328-877D-25	Sequence 25, Appl
61	7	3.1	772	4	US-09-252-991A-31855	Sequence 31855, A
62	7	3.1	803	4	US-09-489-039A-12742	Sequence 12742, A
63	7	3.1	908	4	US-09-635-872A-15	Sequence 15, Appl
64	7	3.1	908	4	US-09-636-077A-15	Sequence 15, Appl
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66	7	3.1	908	4	US-09-986-552-15	Sequence 15, Appl
67	7	3.1	974	4	US-09-636-596C-15	Sequence 15, Appl
68	7	3.1	974	4	US-10-101-464A-921	Sequence 921, App
69	7	3.1	1008	4	US-09-252-991A-29419	Sequence 29419, A
70	7	3.1	1587	4	US-09-845-583A-10	Sequence 10, Appl
71	7	3.1	1587	4	US-09-561-709B-3	Sequence 3, Appl
72	7	3.1	1963	4	US-09-583-110-5243	Sequence 5243, Ap
73	6	2.7	35	3	US-09-014-416-41	Sequence 41, Appl
74	6	2.7	37	4	US-09-732-210-995	Sequence 995, App
75	6	2.7	38	2	US-08-854-222-5	Sequence 5, Appl
76	6	2.7	38	3	US-09-188-039-5	Sequence 5, Appl
77	6	2.7	58	4	US-09-275-252A-25	Sequence 25, Appl
78	6	2.7	59	4	US-09-384-302A-16	Sequence 16, Appl
79	6	2.7	65	4	US-09-328-352-7594	Sequence 7594, Ap
80	6	2.7	67	4	US-09-583-110-4892	Sequence 4892, Ap
81	6	2.7	69	3	US-09-060-726A-7	Sequence 7, Appl
82	6	2.7	72	4	US-09-845-849A-7	Sequence 7, Appl
83	6	2.7	75	3	US-09-227-357-204	Sequence 204, App
84	6	2.7	77	2	US-09-248-796A-16644	Sequence 16644, A
85	6	2.7	79	2	US-07-885-089B-31	Sequence 31, Appl
86	6	2.7	84	4	US-09-828-648-8	Sequence 8, Appl
87	6	2.7	85	1	US-08-341-219-22	Sequence 22, Appl
88	6	2.7	85	3	US-08-912-314A-22	Sequence 22, Appl
89	6	2.7	90	4	US-09-384-302A-17	Sequence 17, Appl
90	6	2.7	93	4	US-09-043-861-4	Sequence 4, Appl
91	6	2.7	100	4	US-09-147-875A-7	Sequence 7, Appl
92	6	2.7	101	2	US-08-710-749-6	Sequence 6, Appl
93	6	2.7	101	4	US-09-621-976-4808	Sequence 4808, Ap
94	6	2.7	104	3	US-09-060-726A-6	Sequence 6, Appl
95	6	2.7	106	4	US-09-489-039A-11876	Sequence 11876, A
96	6	2.7	109	4	US-09-621-976-4312	Sequence 4312, Ap
97	6	2.7	111	4	US-09-252-991A-23343	Sequence 23343, A
98	6	2.7	111	6	5320958-7	Patent No. 5320958
99	6	2.7	113	4	US-09-056-556-230	Sequence 230, App
100	6	2.7	113	4	US-09-072-596-225	Sequence 225, App


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539 6 2.7 928 4 US-09-986-552-1 Sequence 1, Appli
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542 6 2.7 956 4 US-09-252-991A-17124 Sequence 17124, A
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544 6 2.7 963 4 US-09-394-272-13 Sequence 13, Appli
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547 6 2.7 979 3 US-08-878-474-5 Sequence 5, Appli
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549 6 2.7 984 2 US-08-673-789-9 Sequence 9, Appli
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556 6 2.7 1014 4 US-09-252-991A-17583 Sequence 17583, A
557 6 2.7 1021 1 US-08-497-025-3 Sequence 3, Appli
558 6 2.7 1024 4 US-09-562-737-46 Sequence 46, Appli
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560 6 2.7 1029 4 US-09-762-724-6 Sequence 6, Appli
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562 6 2.7 1053 4 US-09-252-991A-19145 Sequence 19145, A
563 6 2.7 1063 1 US-08-093-453B-3 Sequence 3, Appli
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569 6 2.7 1212 3 US-09-090-535-2 Sequence 2, Appli
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575 6 2.7 1307 4 US-09-252-991A-20867 Sequence 20867, A
576 6 2.7 1382 2 US-08-737-715-2 Sequence 2, Appli
577 6 2.7 1382 3 US-09-457-040B-7 Sequence 7, Appli
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579 6 2.7 1430 4 US-09-252-991A-18190 Sequence 18190, A
580 6 2.7 1464 3 US-08-891-640-2 Sequence 2, Appli
581 6 2.7 1495 4 US-09-543-681A-5986 Sequence 5986, Ap
582 6 2.7 1498 4 US-09-252-991A-31234 Sequence 31234, A
583 6 2.7 1498 4 US-09-792-616-9 Sequence 9, Appli
584 6 2.7 1503 3 US-08-976-255-14 Sequence 14, Appli
585 6 2.7 1507 6 5268270-2 Patent No. 5268270
586 6 2.7 1520 4 US-09-252-991A-17501 Sequence 17501, A
587 6 2.7 1560 4 US-09-264-512B-2 Sequence 2, Appli
588 6 2.7 1780 1 US-08-769-309A-5 Sequence 5, Appli
589 6 2.7 1780 2 US-08-994-570-5 Sequence 5, Appli
590 6 2.7 1781 2 US-08-477-451-11 Sequence 11, Appli
591 6 2.7 1781 4 US-09-961-403-13 Sequence 13, Appli
592 6 2.7 1788 2 US-08-962-284-2 Sequence 2, Appli
593 6 2.7 1861 2 US-08-790-912-4 Sequence 4, Appli
594 6 2.7 1956 3 US-08-843-417-10 Sequence 10, Appli
595 6 2.7 1956 4 US-09-527-013-10 Sequence 10, Appli
596 6 2.7 1964 2 US-08-790-912-3 Sequence 3, Appli
597 6 2.7 1965 4 US-09-583-110-3829 Sequence 3829, Ap
598 6 2.7 2052 2 US-08-790-912-2 Sequence 2, Appli
599 6 2.7 2205 1 US-08-093-453B-2 Sequence 2, Appli
600 6 2.7 2285 4 US-09-252-991A-17790 Sequence 17790, A
601 6 2.7 2544 2 US-08-576-626A-32 Sequence 32, Appli
602 6 2.7 2807 4 US-09-543-681A-4980 Sequence 4980, Ap
603 6 2.7 2890 3 US-09-413-814-67 Sequence 67, Appli
604 6 2.7 2892 4 US-08-469-260A-387 Sequence 387, App
605 6 2.7 2892 4 US-08-488-446-387 Sequence 387, App
606 6 2.7 2972 4 US-08-467-344A-387 Sequence 387, App
607 6 2.7 2972 4 US-08-424-550B-387 Sequence 387, App
608 6 2.7 3433 4 US-09-091-501B-10 Sequence 10, Appli
609 6 2.7 3433 4 US-09-538-092-1136 Sequence 1136, Ap
610 6 2.7 3798 3 US-09-335-409-5 Sequence 5, Appli
611 6 2.7 3798 3 US-09-567-969-6 Sequence 6, Appli
612 6 2.7 3798 3 US-09-568-102-6 Sequence 6, Appli
613 6 2.7 3798 3 US-09-568-480-6 Sequence 6, Appli
614 6 2.7 3798 3 US-09-568-486-6 Sequence 6, Appli
615 6 2.7 3798 3 US-09-568-472-6 Sequence 6, Appli
616 6 2.7 3798 3 US-09-567-899-6 Sequence 6, Appli
617 6 2.7 3798 3 US-09-538-092-979 Sequence 979, App
618 6 2.7 5032 4 US-09-335-409-5 Sequence 5, Appli
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621 6 2.7 7257 3 US-09-568-480-5 Sequence 5, Appli
622 6 2.7 7257 3 US-09-568-486-5 Sequence 5, Appli
623 6 2.7 7257 3 US-09-568-472-5 Sequence 5, Appli
624 6 2.7 7257 3 US-09-567-899-5 Sequence 5, Appli
625 6 2.7 7257 3 US-08-714-741-32 Sequence 32, Appli
626 6 2.7 8991 4 US-08-714-741-32 Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-8
; Sequence 8, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -22...-1
US-09-621-976-8

Query Match 94.2%; Score 210; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 2e-195;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYVPELGNIGCKV 60
DB 1 MGWTMLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYVPELGNIGCKV 60
QY 61 VPDCNNYRQKITSNWEPIVKFPGAVDGAATYILVMVYDPDAPSAEPRQRFWRHLVTDIKG 120
DB 61 VPDCNNYRQKITSNWEPIVKFPGAVDGAATYILVMVYDPDAPSAEPRQRFWRHLVTDIKG 120
QY 121 ADLKKGIQCGELSAAYQAPSPAHSGFHYRFFVYVLSQGVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGIQCGELSAAYQAPSPAHSGFHYRFFVYVLSQGVISLLPKENKTRGSKWMDRF 180
QY 181 LNRHFLGPEASTQFMTQYQDSPTLQAPR 210
DB 181 LNRHFLGPEASTQFMTQYQDSPTLQAPR 210

RESULT 2
US-09-513-989C-8
; Sequence 8,'Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
```

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: Patent No. 6783961
:
: FILE REFERENCE: 59.US2.REG
: CURRENT APPLICATION NUMBER: US/09/513,999C
:
: CURRENT FILING DATE: 2000-02-24
:
: PRIOR APPLICATION NUMBER: US 60/122,487
: PRIOR FILING DATE: 1999-03-26
:
: NUMBER OF SEQ ID NOS: 36681
: SOFTWARE: Patent.pm
:
: SEQ ID NO 8
:
: LENGTH: 227
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: SIGNAL
: LOCATION: -22..-1
:
: OTHER INFORMATION: score 8.5
:
: -OTHER INFORMATION: seq AALLGLMMVVTG/DE
: US-09-513-999C-8

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Query Match	94.2%	Score 210;	DB 4;	Length 227;
Best Local Similarity	100.0%;	Pred. No. 2e-195;		
Matches 210;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGWMTRLVTAALLGLMMVVTGDDENSPCAHEALLDDETLFCOGLEVFYPPELGNIGKV	60	
Db	1	MGWMTRLVTAALLGLMMVVTGDDENSPCAHEALLDDETLFCOGLEVFYPPELGNIGKV	60	
QY	61	VPCDNNYRQKITSMPEIVKFPFGAVDGTATILVMVDPDAPSRABPRQRFWRHMLVTDIKG	120	
Db	61	VPCDNNYRQKITSMPEIVKFPFGAVDGTATILVMVDPDAPSRABPRQRFWRHMLVTDIKG	120	
QY	121	ADLKKGKIQCELSAYQAPSPPAHSGFHRVQFFVYLOEGKVISLLPKENKTRGSKWMDRF	180	
Db	121	ADLKKGKIQCELSAYQAPSPPAHSGFHRVQFFVYLOEGKVISLLPKENKTRGSKWMDRF	180	
QY	181	LNRFHIGEPEASTQFMNTQYQDSFTLQAPR	210	
Db	181	LNRFHIGEPEASTQFMNTQYQDSFTLQAPR	210	

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RESULT 3
US-09-208-718-3
; Sequence 3, Application US/09208718
; Patent No. 6063767
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer
; APPLICANT: Corley, Neil
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,820
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749

```

REFERENCE/DOCKET NUMBER: PF-0379 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTU12
CLONE: 3126479
US-09-2008-718-3

Query Match	55.6%	Score 124;	DB 3;	Length 227;
Best Local Similarity	100.0%;	Pred. No. 3.9e-112;		
Matches 124;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGWTRLVTAAALGLMMVVTGDEDENSPCAHEALLDDETLFCOGLSEVFPYELGNIGCKV	60	
Db	1	MGWTRLVTAAALGLMMVVTGDEDENSPCAHEALLDDETLFCOGLSEVFPYELGNIGCKV	60	
Qy	61	VPCNNYRQKITSWMEPIVKFPGAVDGTATILVMVDPAFSRAEPRORFWRHHLVTDIKG	120	
Db	61	VPCNNYRQKITSWMEPIVKFPGAVDGTATILVMVDPAFSRAEPRORFWRHHLVTDIKG	120	
Qy	121	ADLK 124		
Db	121	ADLK 124		

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RESULT 4
US-09-248-796A-21372
; Sequence 21372, Application US/09248796A
; Patent No. 6747137
;
; GENERAL INFORMATION:
;
; APPLICANT: Keith Weinstock et al
;
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO
; ACID COMPOSITIONS FOR DIAGNOSTICS AND THERAPY
;
; FILE REFERENCE: 107196.132
;
; CURRENT APPLICATION NUMBER: US/09/248,796A
;
; CURRENT FILING DATE: 1999-02-12
;
; PRIOR APPLICATION NUMBER: US 60/074,725
;
; PRIOR FILING DATE: 1998-02-13
;
; PRIOR APPLICATION NUMBER: US 60/096,409
;
; PRIOR FILING DATE: 1998-08-13
;
; NUMBER OF SEQ ID NOS: 28208
;
; SEQ ID NO 21372
;
; LENGTH: 116
;
; TYPE: PRT
;
; ORGANISM: Candida albicans
;
; FEATURE:
;
; NAME/KEY: UNSURE
;
; LOCATION: (6),(20)
;
; OTHER INFORMATION: Identity of amino acid
US-09-248-796A-21372

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Query Match	3.6%;	Score 8;	DB 4;	Length 116;
Best Local Similarity	100.0%;	Pred. No. 4.6;		
Matches 8;	Conservative	0;	Mismatches	0;
Indels				Gaps 0;
QY	211	GRASEPKH	218	
Db	43	GRASEPKH	50	

RESULT 5
US-08-974-546-3
; Sequence 3, Application US/08974546
; Patent No. 5945287
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,546
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0428
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRSTNOT18
CLONE: 3172266
US-08-974-546-3

Query Match 3.6%; Score 8; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 LOAPRGA 213
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DB 2 LOAPRGA 9

RESULT 6
US-09-621-976-7099
Sequence 7099, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 7099
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-7099

Query Match 3.6%; Score 8; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 LOAPRGA 213
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DB 2 LOAPRGA 9

RESULT 7
US-09-134-000C-4833
Sequence 4833, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4833
LENGTH: 190
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4833

Query Match 3.6%; Score 8; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 BALDDEDT 40
|||||
DB 27 BALDDEDT 34

RESULT 8
US-08-403-378B-7
Sequence 7, Application US/08403378B
Patent No. 5759991
GENERAL INFORMATION:
APPLICANT: TOHDOH, NAOKI
APPLICANT: TOJO, SHIN-ICHIRO
APPLICANT: KOJIMA, SHIN-ICHI
APPLICANT: UEKI, YASUYUKI
APPLICANT: NISHIHARA, TOSHIO
APPLICANT: FUKUSHIMA, NORIYUKI
APPLICANT: IRIE, TSUNEMASA
APPLICANT: ONO, KEIICHI
APPLICANT: AGUI, HIDEO
APPLICANT: OJIKI, KOSEI
TITLE OF INVENTION: NEUROTROPHIC PEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/403,378B
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-124688
FILING DATE: 27-APR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 1-080398
FILING DATE: 30-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-280590
FILING DATE: 27-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-333241
FILING DATE: 21-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-243003
FILING DATE: 12-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/758,043
FILING DATE: 12-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/873,764
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/01214
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIGGART, WADDELL A
REGISTRATION NUMBER: 24,861
REFERENCE/DOCKET NUMBER:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: rattus norvegicus
STRAIN: wistar
TISSUE TYPE: hippocampal tissue of brain
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-08-403-378B-7

Query Match 3.1%; Score 7; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 DPDAISR 102
DB 8 DPDAISR 14

RESULT 9
US-09-578-063-28
Sequence 28, Application US/09578063
Patent No. 6764677
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A
APPLICANT: Barnes, Thomas M
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 210147.0023/6U1
CURRENT APPLICATION NUMBER: US/09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 22

TYPE: PRT
ORGANISM: Homo sapiens
US-09-578-063-28

Query Match 3.1%; Score 7; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AALLLGL 16
DB 9 AALLLGL 15

RESULT 10
US-09-252-991A-25566
Sequence 25566, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25566
LENGTH: 110
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25566

Query Match 3.1%; Score 7; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AALLLGL 16
DB 14 AALLLGL 20

RESULT 11
US-09-252-991A-29066
Sequence 29066, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29066
LENGTH: 115
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29066

Query Match 3.1%; Score 7; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 APSPPAH 144
DB 94 APSPPAH 100

RESULT 12
US-10-101-464A-618
; Sequence 618, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 618
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-618

Query Match 3.1%; Score 7; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LVTRALL 13
Db 59 LVTAALL 65

RESULT 13
US-09-270-767-43926
; Sequence 43926, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43926
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43926

Query Match 3.1%; Score 7; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 MVDPDP 100
Db 65 MVDPDP 71

RESULT 14
US-07-644-372-2
; Sequence 2, Application US/07644372
; Patent No. 5416009

; GENERAL INFORMATION:
; APPLICANT: Lazzeri, Mario E.
; APPLICANT: Nutman, Thomas B.
; APPLICANT: Weiss, Niklaus
; TITLE OF INVENTION: A DNA SEGMENT ENCODING A SPECIFIC
; TITLE OF INVENTION: IMMUNODIAGNOSTIC ANTIGEN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/644,372
; FILING DATE: 19910123
; CLASSIFICATION: 435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)861-3000
; TELEFAX: (202)822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-644-372-2

Query Match 3.1%; Score 7; DB 1; Length 152;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 DPDPSPR 102
Db 98 DPDPSPR 104

RESULT 15
US-09-208-718-6
; Sequence 6, Application US/09208718
; Patent No. 6063767
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer
; APPLICANT: Corley, Neil
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN PHOSPHOLIPID BINDING PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,820
; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0379 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1143527
; US-09-208-718-6

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Query Match 3.1%; Score 7; DB 3; Length 152;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 96 DPDPSPR 102
Db 53 DPDPSPR 59

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Search completed: January 31, 2005, 15:11:42
Job time : 31 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 15:11:04 ; Search time 154 Seconds
(without alignments)
519.459 Million cell updates/sec

Title: US-10-035-958-61

Perfect score: 223

Sequence: 1 MGMTMLVTAALLGLMMVV.....PTLQAPGRASEPKHKTRQR 223

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Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729239 residues

Word size : 6

Total number of hits satisfying chosen parameters: 5050

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

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2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	223	100.0	223	3	AB18923 A novel p
2	223	100.0	223	5	AAU83707 Human PRO
3	223	100.0	223	5	ABB84969 Human PRO
4	223	100.0	223	5	ABB95575 Human ang
5	223	100.0	223	6	ABU69117 Human PRO
6	223	100.0	223	6	ABU80854 Human PRO
7	223	100.0	223	6	ABO33820 Novel hum
8	223	100.0	223	6	ABO19433 Human sec
9	223	100.0	223	6	ABU69094 Human PRO
10	223	100.0	223	6	ABU82163 Novel hum
11	223	100.0	223	6	ABU81558 Human sec
12	223	100.0	223	6	ADA76586 Novel hum
13	223	100.0	223	6	ABJ72343 Human PRO
14	223	100.0	223	6	ABJ72471 Human PRO
15	223	100.0	223	6	ABO34366 Human sec
16	223	100.0	223	7	ABO25141 Human sec
17	223	100.0	223	7	ABJ72173 Human mem
18	223	100.0	223	7	ABE83722 Novel hum
19	223	100.0	223	7	ABE80828 Novel hum
20	223	100.0	223	7	ABE73369 Novel hum
21	223	100.0	223	7	ABE78451 Novel hum
22	223	100.0	223	7	ABE85099 Human PRO
23	223	100.0	223	7	ABE78205 Novel hum
24	223	100.0	223	7	ABE87271 Human PRO
25	223	100.0	223	7	ABE84853 Human PRO

26	223	100.0	223	7	ADB83968	Novel hum
27	223	100.0	223	7	ADB73123	Novel hum
28	223	100.0	223	7	AAE39111	Human PRO
29	223	100.0	223	7	AAE39048	Human PRO
30	223	100.0	223	7	ADC36961	Human PRO
31	223	100.0	223	7	ADC21951	Human PRO
32	223	100.0	223	7	ADC29817	Novel hum
33	223	100.0	223	7	ADC49982	Novel hum
34	223	100.0	223	7	ADC49181	Novel hum
35	223	100.0	223	7	ADC49698	Novel hum
36	223	100.0	223	7	ADC47559	Novel hum
37	223	100.0	223	7	ADC47304	Novel hum
38	223	100.0	223	7	ADC78179	Novel hum
39	223	100.0	223	7	ADD06414	Novel hum
40	223	100.0	223	7	ADD10595	Human sec
41	223	100.0	223	7	ADC77933	Novel hum
42	223	100.0	223	7	ADD11555	Human sec
43	223	100.0	223	7	ADD50896	Novel hum
44	223	100.0	223	7	ADD51142	Novel hum
45	223	100.0	223	7	ADD37348	Human sec
46	223	100.0	223	7	ADD50623	Human PRO
47	223	100.0	223	7	ADD50377	Human PRO
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50	223	100.0	223	8	ADE21106	Novel hum
51	223	100.0	223	8	ADE05950	Human PRO
52	223	100.0	223	8	ADD75179	Human PRO
53	223	100.0	223	8	ADD75925	Novel hum
54	223	100.0	223	8	ADD85157	Novel hum
55	223	100.0	223	8	ADD86983	Novel hum
56	223	100.0	223	8	ADE20860	Novel hum
57	223	100.0	223	8	ADE39157	Novel hum
58	223	100.0	223	8	ADE05704	Human PRO
59	223	100.0	223	8	ADD73689	Human PRO
60	223	100.0	223	8	ADD78529	Novel hum
61	223	100.0	223	8	ADE41556	Human sec
62	223	100.0	223	8	ADE21352	Novel hum
63	223	100.0	223	8	ADD77467	Novel hum
64	223	100.0	223	8	ADE20614	Novel hum
65	223	100.0	223	8	ADD75679	Human PRO
66	223	100.0	223	8	ADD74195	Human PRO
67	223	100.0	223	8	ADD74441	Human PRO
68	223	100.0	223	8	ADD76171	Novel hum
69	223	100.0	223	8	ADD85663	Novel hum
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71	223	100.0	223	8	ADD75425	Human PRO
72	223	100.0	223	8	ADD76969	Novel hum
73	223	100.0	223	8	ADD86737	Novel hum
74	223	100.0	223	8	ADD78205	Novel hum
75	223	100.0	223	8	ADD77713	Novel hum
76	223	100.0	223	8	ADD77959	Novel hum
77	223	100.0	223	8	ADD85417	Novel hum
78	223	100.0	223	8	ADD73949	Human PRO
79	223	100.0	223	8	ADD74687	Human PRO
80	223	100.0	223	8	ADD77215	Novel hum
81	223	100.0	223	8	ADD85909	Novel hum
82	223	100.0	223	8	ADE05458	Human PRO
83	223	100.0	223	8	ADD74933	Human PRO
84	223	100.0	223	8	ADF09260	Human sec
85	223	100.0	223	8	ADG05745	Novel hum
86	223	100.0	223	8	ADG27299	Human PRO
87	223	100.0	223	8	ADG11362	Novel hum
88	223	100.0	223	8	ADG12141	Novel hum
89	223	100.0	223	8	ADF94698	Novel hum
90	223	100.0	223	8	ADG06794	Human PRO
91	223	100.0	223	8	ADH39138	Novel hum
92	223	100.0	223	8	ADH43739	Human PRO
93	223	100.0	223	8	ADG34228	Novel hum
94	223	100.0	223	8	AD133698	Human PRO
95	223	100.0	223	8	ADH69792	Human PRO
96	223	100.0	223	8	AD139953	Novel hum
97	223	100.0	223	8	ADM27350	Novel hum
98	223	100.0	223	8	ADK83084	Human PRO

PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 09-DEC-1999; 99US-0170262P.
XX (GETH) GENENTECH INC.
PA Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
XX Stewart TA, Watanabe CK, Wood WI, Zhang Z;
PI WPI; 2000-628263/60.
XX N-PSDB; AAA96350.
DR Novel secreted and transmembrane polypeptides useful for diagnosing tumor
PT in a mammal, for identifying agonists and antagonists of the polypeptide
PT and for therapeutic use.
XX Claim 12; Fig 30; 222pp; English.
XX The present sequence represents a secreted or transmembrane polypeptide.
CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4435, PRO5990,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumor in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells and
CC are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing
XX Sequence 223 AA;
SQ Query Match 100.0%; Score 223; DB 3; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214; Indels 0; Gaps 0;
Matches 223; Conservative 0; Mismatches 0;
QY 1 MGWTVRLVTAALLGLMVMVVTGDENSPCAHEALLDEDTLFCQGLEVFYPGLGNIGCKV 60
Db 1 MGWTVRLVTAALLGLMVMVVTGDENSPCAHEALLDEDTLFCQGLEVFYPGLGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMEPIVKFPGVDGATYILVMVDPDAPSAEPQRQFRRHMLVTDIKG 120
Db 61 VPDCCNNYRQKITSWMEPIVKFPGVDGATYILVMVDPDAPSAEPQRQFRRHMLVTDIKG 120
QY 121 ADLKKGKIQGELSAYQAPSPPAHSGFHYQPFVYLQBGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKKGKIQGELSAYQAPSPPAHSGFHYQPFVYLQBGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGSPEASTQFTWNTQYQDSPTLQAPRGASEPKHKTRQ 223
Db 181 LNRFLHGSPEASTQFTWNTQYQDSPTLQAPRGASEPKHKTRQ 223
RESULT 2
AAU83707
ID AAU83707 standard; protein; 223 AA.
XX AC AAU83707;
XX DT 08-MAY-2002 (first entry)
XX Human PRO protein, Seq ID No 232.
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;

KW tumour necrosis factor-alpha.
XX Homo sapiens.
XX WO2000208288-A2.
XX 31-JAN-2002.
XX 29-JUN-2001; 2001WO-US021066.
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220585P.
XX 25-JUL-2000; 2000US-0220605P.
XX 25-JUL-2000; 2000US-0220607P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220638P.
XX 25-JUL-2000; 2000US-0220664P.
XX 25-JUL-2000; 2000US-0220666P.
XX 26-JUL-2000; 2000US-0220893P.
XX 28-JUL-2000; 2000WO-US020710.
XX 01-AUG-2000; 2000US-0222425P.
XX 22-AUG-2000; 2000US-0227133P.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 10-NOV-2000; 2000WO-US030873.
XX 28-NOV-2000; 2000US-0253646P.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.
XX 22-MAR-2001; 2001US-00816744.
XX 10-MAY-2001; 2001US-00854208.
XX 25-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001WO-US017092.
PA (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen MB, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
DR N-PSDB; ABK33651.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX Claim 11; Fig 232; 359pp; English.
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumors, especially lung
CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
CC liver tumor. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX Sequence 223 AA;
SQ Query Match 100.0%; Score 223; DB 5; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214; Indels 0; Gaps 0;
Matches 223; Conservative 0; Mismatches 0;


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QY 1 MGWTMLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYYPGLGNIGCKV 60
Db 1 MGWTMLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYYPGLGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGGATYILVMVDDPAPSAEPRQRFWRHVLVTDIKG 120
Db 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGGATYILVMVDDPAPSAEPRQRFWRHVLVTDIKG 120
QY 121 ADLKKGKIQQELSAYQAPSPPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKKGKIQQELSAYQAPSPPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223
Db 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 3
ABB84969
ID ABB84969 standard; protein; 223 AA.
XX
AC ABB84969;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO4408 protein sequence SEQ ID NO:306.
XX
KW Human; angiogenesis; cardiac; cystostatic; antiangiogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial stenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US019692.
XX
PR 23-JUN-2000; 2000US-0213637P.
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
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PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritson ME, Goddard A;
PI Godowski BJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
XX N-PSDB; ABL88224.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 306; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
XX antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
XX cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,
XX angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The PRO polynucleotides have applications in molecular biology,
XX including use as hybridisation probes, and in chromosome and gene
XX mapping. ABL88259 to ABL88267 represent primers and probes used in the
XX exemplification of the present invention
XX
XX Sequence 223 AA;
XX
XX Query Match 100.0%; Score 223; DB 5; Length 223;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-214; Mismatches 0; Gaps 0;
XX Matches 223; Conservative 0; Indels 0;
XX
QY 1 MGWTMLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYYPGLGNIGCKV 60
Db 1 MGWTMLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYYPGLGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGGATYILVMVDDPAPSAEPRQRFWRHVLVTDIKG 120
Db 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGGATYILVMVDDPAPSAEPRQRFWRHVLVTDIKG 120
QY 121 ADLKKGKIQQELSAYQAPSPPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKWMDRF 180
Db 121 ADLKKGKIQQELSAYQAPSPPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223
Db 181 LNRFLHGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 4
ABB95575
ID ABB95575 standard; protein; 223 AA.
XX
AC ABB95575;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human angiogenesis related protein PRO4408 SEQ ID NO: 306.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
XX
```

KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
XX antiarteriosclerotic.

OS Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US021735.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00643657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242522P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00767609.

XX 28-FEB-2001; 2001US-00796498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00808689.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 25-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866038.

XX 25-MAY-2001; 2001US-00866034.

XX 30-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017443.

XX 20-JUN-2001; 2001WO-US017800.

XX 20-JUN-2001; 2001WO-US019692.

PI (BAKE/) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERB/) GERBER H.

PA (GERP/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (MARS/) MARSTERS S A.

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PA (MARS/) MARSTERS S A.

PA (MARS/) MARSTERS S A.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-171999/22.

XX N-PSDB; ABL95713.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 306; 567pp; English.

XX The present invention provides the protein and coding sequences of human
XX PRO proteins. These are useful for treating or diagnosing a
XX cardiovascular, endothelial or angiogenic disorder, including cardiac
XX hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumor
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The present sequence is a PRO protein of the invention

SQ Sequence 223 AA;

Query Match 100.0%; Score 223; DB 5; Length 223;

Best Local Similarity 100.0%; Pred. No. 3.5e-214;

Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGTWRLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYPGLNIGCKV 60

Db 1 MGTWRLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYPGLNIGCKV 60

Qy 61 VPCNNYRQKITSWMEPIVKFPGAVDGYTILVMVDPDAPSAEPRQRFWRHLVTDIKG 120

Db 61 VPCNNYRQKITSWMEPIVKFPGAVDGYTILVMVDPDAPSAEPRQRFWRHLVTDIKG 120

Qy 121 ADLKGKIQGQELSAQAPSPAHSGFHYQFFVYLQEGKVISLLPKENKTRGSKMDRF 180

Db 121 ADLKGKIQGQELSAQAPSPAHSGFHYQFFVYLQEGKVISLLPKENKTRGSKMDRF 180

Qy 181 LNRFHGLGEPEASTQFTMTQNYQDSPTLOAPGRASEPKHKTRQ 223

Db 181 LNRFHGLGEPEASTQFTMTQNYQDSPTLOAPGRASEPKHKTRQ 223

RESULT 5

ABU69117

ID ABU69117 standard; protein; 223 AA.

XX AC ABU69117;

XX DT 02-JUN-2003 (first entry)

XX DE Human PRO polypeptide #15.

XX KW Human; secreted and transmembrane protein; bone disorder; obesity;

XX KW cartilage disorder; sports injury; arthritis; diabetes mellitus;

XX KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassaemia;

XX KW haemoglobin-associated disorder; kidney disorder; Berger disease;

XX KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;

XX KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;

XX KW antiarthritic; antidiabetic; antianaemic; nephrotropic; antiinflammatory.

XX OS Homo sapiens.

XX PN US2003032061-A1.

XX PD 13-FEB-2003.

XX PF 26-DEC-2001; 2001US-00036214.

XX PR 15-MAY-1998; 98US-0085579P.

XX PR 15-DEC-1998; 98US-0112514P.

XX PR 22-DEC-1998; 98US-0113300P.

XX PR 23-DEC-1998; 98US-0113430P.

XX PR 23-DEC-1998; 98US-0113605P.

XX PR 23-DEC-1998; 98US-0113621P.

XX PR 23-DEC-1998; 98US-0114140P.

XX PR 12-JAN-1999; 99US-0115552P.

XX PR 22-JAN-1999; 99US-0116843P.

XX PR 23-MAR-1999; 99US-0125774P.

XX PR 23-MAR-1999; 99US-0125778P.

PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 14-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99US-0132383P.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99US-028551.
PR 22-DEC-1999; 99US-028551.
PR 01-MAR-2000; 2000US-0030720.
PR 02-MAR-2000; 2000US-0030720.
PR 22-MAY-2000; 2000US-0030720.
PR 02-JUN-2000; 2000US-0030720.
PR 23-AUG-2000; 2000US-0030720.
PR 24-AUG-2000; 2000US-0030720.
PR 01-DEC-2000; 2000US-0030720.
PR 28-FEB-2001; 2001US-0030720.
PR 01-JUN-2001; 2001US-0030720.
PR 20-JUN-2001; 2001US-0030720.
PR 09-JUL-2001; 2001US-0030720.
PR 16-AUG-2001; 2001US-0030720.
XX (GETH) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-341962/32.
XX N-PSDB; ACA06170.
XX
XX Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,
PT PRO1887, PRO1785, PRO4333, useful for treating sports injuries,
PT arthritis, diabetes, obesity, hyper- or hypo-insulinemia.
XX
XX Claim 12; Fig 30; 194pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful in diagnosing or treating
CC various bone and/or cartilage disorders (e.g. sports injuries,
CC arthritis), various insulin deficient states (e.g. diabetes mellitus,
CC hypo-insulinemia), obesity, hyper-insulinemia, haemoglobin-associated
CC disorders (e.g. thalassemias), kidney disorders associated with
CC decreased mesangial cell function (e.g. Berger disease), or other
CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,
CC dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide
CC sequences may be used as hybridisation probes in chromosome and gene
CC mapping, or in generating antisense RNA and DNA. They are also useful in
CC preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, to generate transgenic animals or
CC knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification, and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO polypeptides, or for the affinity
CC purification of the polypeptides from recombinant cell culture or natural
CC sources. ABU69103-ABU69125 represent the human PRO polypeptides of the
CC invention

SQ Sequence 223 AA;
Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDDTLFCQGLEVFYFELGNIGCKV 60
DB 1 MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDDTLFCQGLEVFYFELGNIGCKV 60
QY 61 VPDCCNRYRQKITSWMEPIVKFPGAVDGTATYILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
DB 61 VPDCCNRYRQKITSWMEPIVKFPGAVDGTATYILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
QY 121 ADLKKGIQGGELSAQAPSPAHSGFHRHYOFFVYVYQEGKVISLIPKENTKRGSKWDRF 180
DB 121 ADLKKGIQGGELSAQAPSPAHSGFHRHYOFFVYVYQEGKVISLIPKENTKRGSKWDRF 180
QY 181 LNRFHLPGEPEASTQFMNTQYQDSPTLQAPGRASEPKHKTRQR 223
DB 181 LNRFHLPGEPEASTQFMNTQYQDSPTLQAPGRASEPKHKTRQR 223
RESULT 6
ASU80854
ID ASU80854 standard; protein; 223 AA.
XX
XX AC ASU80854;
XX
XX DT 23-JUN-2003 (first entry)
XX
XX DE Human PRO polypeptide #116.
XX
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN US2003036635-A1.
XX
XX PD 20-FEB-2003.
XX
XX PF 28-AUG-2002; 2002US-00230163.
XX
XX PR 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
XX
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-342045/32.
XX N-PSDB; ACA66956.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
XX Claim 11; Fig 232; 314pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC specific in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ABU80739-ABU80860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the

```
CC USPTO web site at seqdata.uspto.gov/psipspidEntry.html
XX
SQ Sequence 223 AA;

Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWTMLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
DB 1 MGWTMLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60

QY 61 VPDCNNYRKITSWMEPIVKFPGAVDGYIILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
DB 61 VPDCNNYRKITSWMEPIVKFPGAVDGYIILVMVDPDAPSAEPRQRFWRHLVTDIKG 120

QY 121 ADLKGKIQGELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQGELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180

QY 181 LNRHFLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRHFLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 7
ABO33820
ID ABO33820 standard; protein; 223 AA.
XX
AC ABO33820;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO4408.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
colon tumour; breast tumour; prostate tumour; rectal tumour;
liver tumour; bone disorder; cartilage disorder; sports injury;
arthritis; wound.
XX
OS Homo sapiens.
XX
PN US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-512315/48.
DR N-PSDB; ACD68708.
XX
XX New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte, or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX
XX Claim 11; Fig 232; 314pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
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CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 223 AA;

Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWTMLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
DB 1 MGWTMLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60

QY 61 VPDCNNYRKITSWMEPIVKFPGAVDGYIILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
DB 61 VPDCNNYRKITSWMEPIVKFPGAVDGYIILVMVDPDAPSAEPRQRFWRHLVTDIKG 120

QY 121 ADLKGKIQGELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQGELSAYQAPSPAHSGFHRFYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180

QY 181 LNRHFLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRHFLGEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 8
ABO19433
ID ABO19433 standard; protein; 223 AA.
XX
AC ABO19433;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human secreted / transmembrane polypeptide PRO4408.
XX
KW Human; gene therapy; diabetes; obesity; hypoinulinaemia.
XX
OS Homo sapiens.
XX
PN US2003027249-A1.
XX
PD 06-FEB-2003.
XX
PF 16-AUG-2001; 2001US-00931836.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
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PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127708P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-00311832.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138168P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 25-AUG-1999; 99US-00380142.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99US-0028551.
PR 22-DEC-1999; 99US-0030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000US-00644848.
PR 23-AUG-2000; 2000US-0023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001US-00869599.
PR 29-JUN-2001; 2001WO-US021086.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
XX
XX (GETH ) GENENTECH INC.
PA
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
PI
XX WPI; 2003-492030/46.
DR N-PSDB; ACD28839.
XX
XX New isolated, secreted and transmembrane PRO polypeptides and encoding
PT nucleic acids, useful for the diagnosis and treatment of disorders such
PT as diabetes, obesity and/or hypoinulinemia.
XX
XX Claim 12; Fig 30; 196pp; English.
XX
CC The invention relates to a new isolated nucleic acid which encodes a PRO
CC polypeptide. The methods and compositions of the present invention are
CC useful for the diagnosis and treatment of disorders associated with the
CC PRO polypeptides, such as diabetes, obesity and hypoinulinemia. The
CC present sequence represents the amino acid sequence of a human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 223 AA;

Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.58-214;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US019692.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX (GETH) GENENTECH INC.
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
PI N-PSDB; ACA06113.
DR WPI; 2003-341326/32.
XX N-PSDB; ACA06113.
XX New PRO polypeptides and nucleic acid molecules, useful for diagnosing or
PT treating diabetes mellitus, cancers, septic shock, inflammatory bowel
PT disease or asthma, or in gene therapy, chromosome identification or
PT tissue typing.
XX Claim 12; Fig 30; 196pp; English.
PS The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful in diagnosing or treating non
CC -insulin dependent diabetes mellitus, cancers, septic shock, rheumatoid
CC arthritis, graft-versus-host disease, stroke, cardiac ischaemia,
CC psoriasis, inflammatory bowel disease or asthma. The PRO polynucleotide
CC sequences may be used as hybridisation probes in chromosome and gene
CC mapping, or in generating antisense RNA and DNA. They are also useful in
CC preparing PRO polypeptides, in assays to identify other proteins or
CC molecules involved in binding reaction, to generate transgenic animals or
CC knockout animals, which in turn are useful in the development and
CC screening of therapeutically useful reagents, for chromosome
CC identification, and tissue typing. The PRO polypeptides and nucleic acid
CC molecules are also useful in gene therapy, and as molecular weight
CC markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC used in diagnostic assays for PRO polypeptides, or for the affinity
CC purification of the polypeptides from recombinant cell culture or natural
CC sources. ABU69080-ABU69102 represent the human PRO polypeptides of the
XX invention
SQ Sequence 223 AA;
Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214; Mismatches 0; Indels 0; Gaps 0;
Matches 223; Conservative 0;
QY 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
DB 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMEPIVKFPGVDGATYILVMVDPDAPRAEPQRQFWRHVLVTDIKG 120
DB 61 VPDCCNNYRQKITSWMEPIVKFPGVDGATYILVMVDPDAPRAEPQRQFWRHVLVTDIKG 120
QY 121 ADLKKGKIQGQELSAQAPSPAHSGFHHYOFFVYLQEGKVISLIPKENKTRGSKWDRF 180
DB 121 ADLKKGKIQGQELSAQAPSPAHSGFHHYOFFVYLQEGKVISLIPKENKTRGSKWDRF 180
QY 181 LNRFLGPEASTQPMQTQYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRFLGPEASTQPMQTQYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 10
ABU82163
ID ABU82163 standard; protein; 223 AA.
XX AC ABU82163;
XX DT 25-JUN-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO4408.
XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW antiangiogenic; hypotensive; vulnery; antiatherosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX Homo sapiens.
OS US2003088063-A1.
XX PN 08-MAY-2003.
XX PD 12-AUG-2002; 2002US-00219003.
XX PF 25-JUL-2000; 2000US-0220664P.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen MB, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-393229/37.
XX N-PSDB; ACA68612.
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX Claim 11; Fig 232; 314pp; English.
CC The invention describes one hundred and eighty seven nucleic acids
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC treating or diagnosing a cardiovascular, endothelial or angiogenic
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC related macular degeneration, atherosclerosis, hypertension, arterial
CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridisation
CC probes, and in chromosome and gene mapping. This is the amino acid
CC sequence of a novel human secreted and transmembrane PRO polypeptide
XX Sequence 223 AA;
Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214; Mismatches 0; Indels 0; Gaps 0;
Matches 223; Conservative 0;
QY 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
DB 1 MGWTRLVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMEPIVKFPGVDGATYILVMVDPDAPRAEPQRQFWRHVLVTDIKG 120
DB 61 VPDCCNNYRQKITSWMEPIVKFPGVDGATYILVMVDPDAPRAEPQRQFWRHVLVTDIKG 120

```
QY 121 ADLKKGKIQQGELSAYQAPSPPAHSGFHRYOFFVYLQSGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGKIQQGELSAYQAPSPPAHSGFHRYOFFVYLQSGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFMNTQNYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRFLHGEPEASTQFMNTQNYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 11
ABU81558
ID ABU81558 standard; protein; 223 AA.
AC ABU81558;
XX
XX 24-JUN-2003 (first entry)
XX
XX Human secreted polypeptide PRO4408.
XX
XX Human; inflammatory disease; organ failure; atherosclerosis; cancer;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW differentiation disorder; cell adhesion disorder; skin disorder;
KW neural receptor disorder; diabetic complication; tissue typing.
XX
XX Homo sapiens.
OS
XX
XX US2002192751-A1.
XX
XX 19-DEC-2002.
XX
XX 26-DEC-2001; 2001US-00036041.
XX
XX 15-MAY-1998; 98US-0085579P.
XX
XX 15-DEC-1998; 98US-0112514P.
XX
XX 22-DEC-1998; 98US-0113300P.
XX
XX 23-DEC-1998; 98US-0113430P.
XX
XX 23-DEC-1998; 98US-0113605P.
XX
XX 23-DEC-1998; 98US-0113621P.
XX
XX 23-DEC-1998; 98US-0114140P.
XX
XX 12-JAN-1999; 99US-0115552P.
XX
XX 22-JAN-1999; 99US-0116843P.
XX
XX 23-MAR-1999; 99US-0125774P.
XX
XX 23-MAR-1999; 99US-0125778P.
XX
XX 24-MAR-1999; 99US-0125826P.
XX
XX 31-MAR-1999; 99US-0127035P.
XX
XX 05-APR-1999; 99US-0127066P.
XX
XX 13-APR-1999; 99US-0129122P.
XX
XX 21-APR-1999; 99US-0130359P.
XX
XX 27-APR-1999; 99US-0131270P.
XX
XX 27-APR-1999; 99US-0131272P.
XX
XX 27-APR-1999; 99US-0131291P.
XX
XX 04-MAY-1999; 99US-0132371P.
XX
XX 04-MAY-1999; 99US-0132379P.
XX
XX 04-MAY-1999; 99US-0132383P.
XX
XX 14-MAY-1999; 99US-0132703P.
XX
XX 25-MAY-1999; 99US-0135750P.
XX
XX 08-JUN-1999; 99US-0138166P.
XX
XX 20-JUL-1999; 99US-0144791P.
XX
XX 03-AUG-1999; 99US-0146970P.
XX
XX 29-OCT-1999; 99US-0162506P.
XX
XX 02-DEC-1999; 99US-0162551P.
XX
XX 22-DEC-1999; 99US-0162551P.
XX
XX 01-MAR-2000; 2000US005601.
XX
XX 02-MAR-2000; 2000US005841.
XX
XX 22-MAY-2000; 2000US014042.
XX
XX 02-JUN-2000; 2000US015284.
XX
XX 23-AUG-2000; 2000US023522.
XX
XX 24-AUG-2000; 2000US023328.
XX
XX 01-DEC-2000; 2000US032678.
XX
XX 20-DEC-2000; 2000US034956.
XX
XX 28-FEB-2001; 2001US0006520.
XX
XX 01-JUN-2001; 2001US0017800.
XX
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PR 20-JUN-2001; 2001US019592.
PR 29-JUN-2001; 2001US021066.
PR 09-JUL-2001; 2001US021735.
PR 16-AUG-2001; 2001US-00931836.
XX
XX (GETH ) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-341079/32.
XX
XX N-PSDB; ACA67736.
XX
XX New secreted and transmembrane nucleic acids and polypeptides, designated
PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT cancer.
XX
XX Claim 12; Fig 30; 195pp; English.
XX
XX The invention relates to an isolated nucleic acid that encodes a PRO
CC polypeptide. The nucleic acids and polypeptides are useful for treating
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC infertility, birth defects, premature aging, acquired immunodeficiency
CC syndrome (AIDS), cancer, differentiation disorders, cell adhesion
CC disorders, neural receptor disorders, skin disorders or diabetic
CC complications. The nucleic acids are useful as hybridisation probes, in
CC chromosome and gene mapping and in generating antisense RNA or DNA. The
CC polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. Both are useful in tissue typing. The present sequence
CC represents the amino acid sequence of a PRO polypeptide of the invention
XX
XX Sequence 223 AA;
SQ
Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGWTMLRVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
DB 1 MGWTMLRVTAALLGLMMVVTGDENSPCAHEALLDEDTLFCQGLEVFYFELGNIGCKV 60
QY 61 VPCNNYRQKITSWMEPIVKFPGAVDGTATYILVMVDPDAPRAEPQRQFWRHLVTDIKG 120
DB 61 VPCNNYRQKITSWMEPIVKFPGAVDGTATYILVMVDPDAPRAEPQRQFWRHLVTDIKG 120
QY 121 ADLKKGKIQQGELSAYQAPSPPAHSGFHRYOFFVYLQSGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGKIQQGELSAYQAPSPPAHSGFHRYOFFVYLQSGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFLHGEPEASTQFMNTQNYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRFLHGEPEASTQFMNTQNYQDSPTLQAPRGRASEPKHKTRQ 223

RESULT 12
ADA76586
ID ADA76586 standard; protein; 223 AA.
XX
XX ADA76586;
XX
XX 20-NOV-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO4408.
XX
XX human; secreted and transmembrane protein; PRO; tumour; gene therapy;
KW tissue typing; chromosome identification; cytostatic.
XX
XX Homo sapiens.
XX
XX US2003036114-A1.
XX
XX 20-FEB-2003.
XX
XX
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XX 26-DEC-2001; 2001US-00035719.
XX
XX
XX 15-MAY-1998; 98US-0085579P.
XX 15-DEC-1998; 98US-0112514P.
XX 22-DEC-1998; 98US-0113300P.
XX 23-DEC-1998; 98US-0113430P.
XX 23-DEC-1998; 98US-0113605P.
XX 23-DEC-1998; 98US-0113621P.
XX 23-DEC-1998; 98US-0114140P.
XX 12-JAN-1999; 99US-0115552P.
XX 22-JAN-1999; 99US-0116843P.
XX 23-MAR-1999; 99US-0125774P.
XX 23-MAR-1999; 99US-0125778P.
XX 24-MAR-1999; 99US-0125826P.
XX 31-MAR-1999; 99US-0127033P.
XX 05-APR-1999; 99US-0127708P.
XX 13-APR-1999; 99US-0129122P.
XX 21-APR-1999; 99US-0130359P.
XX 27-APR-1999; 99US-0131270P.
XX 27-APR-1999; 99US-0131272P.
XX 27-APR-1999; 99US-0131291P.
XX 04-MAY-1999; 99US-0132371P.
XX 04-MAY-1999; 99US-0132379P.
XX 04-MAY-1999; 99US-0132383P.
XX 14-MAY-1999; 99US-0132383P.
XX 25-MAY-1999; 99US-0135750P.
XX 08-JUN-1999; 99US-0138166P.
XX 20-JUL-1999; 99US-0144791P.
XX 03-AUG-1999; 99US-0146970P.
XX 29-OCT-1999; 99US-0162506P.
XX 02-DEC-1999; 99US-0208551.
XX 22-DEC-1999; 99US-0307020.
XX 01-MAR-2000; 2000US-0005601.
XX 02-MAR-2000; 2000US-0005841.
XX 22-MAY-2000; 2000US-0014042.
XX 02-JUN-2000; 2000US-0015264.
XX 23-AUG-2000; 2000US-0023522.
XX 24-AUG-2000; 2000US-0023328.
XX 01-DEC-2000; 2000US-0032678.
XX 20-DEC-2000; 2000US-0034956.
XX 28-FEB-2001; 2001US-0006520.
XX 01-JUN-2001; 2001US-0017800.
XX 20-JUN-2001; 2001US-0019692.
XX 29-JUN-2001; 2001US-0021066.
XX 09-JUL-2001; 2001US-0021735.
XX 16-AUG-2001; 2001US-00931836.
XX
XX (GETH) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
XX Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-615764/58.
XX N-PSDB; ADA76585.
XX
XX Novel isolated secreted and transmembrane polypeptides, designated as PRO
XX polypeptides e.g. PRO1484, PRO4334 and PRO1122, useful for inhibiting
XX tumor cell growth, and for preparing medicaments for therapeutic use.
XX
XX Claim 12; Fig 30; 201pp; English.
XX
XX The invention describes an isolated secreted and transmembrane PRO
XX polypeptide (I), having at least 80% identity to or scoring at least 80%
XX positives when compared to a sequence (S1) comprising 246, 440, 197, 97,
XX 273, 571, 209, 888, 502, 310, 251, 800, 507, 248, 223, 134, 136, 468,
XX 328, 221, 194, 899, or 339 amino acids fully defined in the
XX specification. An anti-(I)-antibody is useful for determining the
XX presence of (I) in a cell. (I) is useful for identifying a compound
XX capable of inhibiting the expression and/or activity of (I). (I) and the
XX antibody are useful for inhibiting the growth of tumor cells, and for
XX the preparation of a medicament useful in the treatment of a condition
XX which is responsive to (I) or the antibody. A polynucleotide (II)

CC encoding (I) is also useful for isolating full-length PRO cDNA for
CC generating transgenic animals or knock-out animals, which are, in turn,
CC are useful in the development in the screening of therapeutically useful
CC reagents, and in gene therapy. PRO is useful in assays to identify other
CC proteins or molecules involved in binding interactions, for screening
CC inhibitors or agonists of binding interactions and for screening chemical
CC libraries. (I) is useful as molecular weight marker for protein
CC electrophoresis, and as therapeutic agents. (I) or (II) is useful for
CC tissue typing and for chromosome identification. Ab is useful in
CC diagnostic assays for PRO, in affinity purification of PRO, and for
CC detection of PRO in biological samples. This is the amino acid sequence
XX of a novel human secreted and transmembrane PRO polypeptide.
XX
XX Sequence 223 AA;
XX
XX Query Match 100.0%; Score 223; DB 6; Length 223;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-214; Indels 0; Gaps 0;
XX Matches 223; Conservative 0; Mismatches 0;
XX
XX QY 1 MGWTMRLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGKV 60
XX DB 1 MGWTMRLVTAALLGLMMVVTGDEENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGKV 60
XX
XX QY 61 VPDCCNRYRQKITSWMEPIVKFPGAVDGYATYILVMVDPDAPRAEPQRQFWRHLVTDIK 120
XX DB 61 VPDCCNRYRQKITSWMEPIVKFPGAVDGYATYILVMVDPDAPRAEPQRQFWRHLVTDIK 120
XX
XX QY 121 ADLKKGIQOQELSAQAPSPAHSGFHYOFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
XX DB 121 ADLKKGIQOQELSAQAPSPAHSGFHYOFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
XX
XX QY 181 LNRPHLGEPEASTQFMQYQDSPTLQAPRGRASEPKHKTQR 223
XX DB 181 LNRPHLGEPEASTQFMQYQDSPTLQAPRGRASEPKHKTQR 223
XX
XX RESULT 13
XX ABJ72343
XX ID ABJ72343 standard; protein; 223 AA.
XX
XX AC ABJ72343;
XX
XX DT 06-NOV-2003 (first entry)
XX
XX DE Human PRO4408 protein.
XX
XX KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
XX differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX
XX OS Homo sapiens.
XX
XX PN US2003050448-A1.
XX
XX PD 13-MAR-2003.
XX
XX PF 28-AUG-2002; 2002US-002304114.
XX
XX PR 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-521818/49.
XX N-PSDB; ABT4341.
XX
XX New nucleic acid encoding for a PRO protein, useful for the manufacture
XX of a medicament for diagnosing or treating tumors or for measuring or
XX detecting expression of an associated gene.
XX

PS Claim 11; Fig 232; 315pp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding a fully defined PRO polypeptide. The molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells or the release of TNF-alpha from human blood. Other possible uses include the stimulation or inhibition of chondrocyte proliferation or differentiation and the stimulation of human dermal fibroblast cell proliferation and the detection of the presence of a tumour within a mammal. Furthermore, the nucleic acid may be useful for the manufacture of a medicament for diagnosing or treating a tumour within a mammal or for measuring or detecting the expression of an associated gene, as well as during gene therapy. The current sequence is that of the human PRO protein of the invention
XX
XX
SQ Sequence 223 AA;
Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214; Mismatches 0; Indels 0; Gaps 0;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHLVTDIKG 120
DB 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHLVTDIKG 120
QY 121 ADLKKGKIQQGELSAYQAPSPPAHSGFHRYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGKIQQGELSAYQAPSPPAHSGFHRYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRHFLGPEASTQFMNTQYQDSPTLQAPGRASEPKHKTRQ 223
DB 181 LNRHFLGPEASTQFMNTQYQDSPTLQAPGRASEPKHKTRQ 223
RESULT 14
ABJ72471
ID ABJ72471 standard; protein; 223 AA.
XX
AC ABJ72471;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO4408 protein.
XX
KW PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KW tumour necrosis factor; proliferation; differentiation; gene therapy;
KW dermal fibroblast.
XX
OS Homo sapiens.
XX
PN US2003027988-A1.
XX
PD 06-FEB-2003.
XX
PF 26-AUG-2002; 2002US-00227884.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-503301/47.
DR N-PSDB; ABT44624.
XX
PT New PRO protein encoding nucleic acid, useful for preparing PRO

PT polypeptides and anti-PRO antibodies for detecting the presence of a tumor in a mammal.
XX
XX Claim 11; Fig 232; 324pp; English.
XX
CC The invention relates to a novel isolated PRO protein encoding nucleic acid. The nucleic acid of the invention may be useful for preparing PRO polypeptides and anti-PRO antibodies for detecting the presence of a tumor in a mammal. Furthermore, the molecules of the invention may be useful for stimulating proliferation or gene expression in pericyte cells, the release of tumour necrosis factor (TNF)-alpha from human blood, the proliferation or differentiation of chondrocyte cells and for inhibiting the proliferation of normal human dermal fibroblast cells.
CC Finally, the molecules may be utilised during gene therapy. The current sequence is that of the human PRO protein of the invention
XX
XX
SQ Sequence 223 AA;
Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214; Mismatches 0; Indels 0; Gaps 0;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHLVTDIKG 120
DB 61 VPDCCNNYRQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSRAEPRQRFWRHLVTDIKG 120
QY 121 ADLKKGKIQQGELSAYQAPSPPAHSGFHRYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKKGKIQQGELSAYQAPSPPAHSGFHRYQFFVYLOEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRHFLGPEASTQFMNTQYQDSPTLQAPGRASEPKHKTRQ 223
DB 181 LNRHFLGPEASTQFMNTQYQDSPTLQAPGRASEPKHKTRQ 223
RESULT 15
ABO34366
ID ABO34366 standard; protein; 223 AA.
XX
AC ABO34366;
XX
DT 19-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO 4405.
XX
KW Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
KW human dermal fibroblast stimulation; tumour; tissue typing;
KW affinity purification.
XX
OS Homo sapiens.
XX
PN US200304934-A1.
XX
PD 06-MAR-2003.
XX
PF 28-AUG-2002; 2002US-00230338.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-492274/46.
DR N-PSDB; ACD82291.
XX

PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 19; Fig 232; 315pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. Nucleic acids that encode PRO can be used to generate either
CC transgenic animals or knock-out animals useful in developing and
CC screening of therapeutically useful reagents. The nucleic acids may also
CC be used in gene therapy for replacing defective gene, in chromosome
CC identification, as chromosome markers, or in generating probes to isolate
CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
CC stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
CC and for detecting the presence of tumour in an animal. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The present sequence represents the amino acid sequence
CC of a human secreted/transmembrane PRO polypeptide
XX
SQ Sequence 223 AA;

Query Match 100.0%; Score 223; DB 6; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.5e-214; Mismatches 0; Gaps 0;
Matches 223; Conservative 0; Indels 0; Gaps 0;
QY 1 MGMTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
DB 1 MGMTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYFPELGNIGCKV 60
QY 61 VPDCCNRYQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
DB 61 VPDCCNRYQKITSWMEPIVKFPGAVDGYIILVMVDPDAPSAEPRQRFWRHLVTDIKG 120
QY 121 ADLKGKIQGQELSAVQAPSPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKWMDRF 180
DB 121 ADLKGKIQGQELSAVQAPSPAHSGFHRYPFVYLQEGKVISLLPKENKTRGSKWMDRF 180
QY 181 LNRFHLEPEASTQFMVTQNYQDSPTLQAPRGRASEPKHKTRQ 223
DB 181 LNRFHLEPEASTQFMVTQNYQDSPTLQAPRGRASEPKHKTRQ 223

Search completed: January 31, 2005, 15:17:05
Job time : 228 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 15:11:04 ; Search time 16 Seconds
(without alignments)
1341.021 Million cell updates/sec

Title: US-10-035-958-61
Perfect score: 223
Sequence: 1 MGWTRLVTAALLGLMMV.....PTLQAPRGRASEPKHKTRQR 223

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 979

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.6	319	2 AH1247	hypothetical prote
2	8	3.6	439	2 F84278	3-phosphoshikimate
3	8	3.6	1551	1 A43364	M polypeptide
4	7	3.1	24	2 S10682	cytochrome P450 is
5	7	3.1	24	2 S10681	probable 7-ethoxyc
6	7	3.1	26	2 A61056	aminopyrine N-deme
7	7	3.1	26	2 B44107	cytochrome P450 NF
8	7	3.1	28	2 S29135	aminopyrine N-deme
9	7	3.1	28	2 S29136	aminopyrine N-deme
10	7	3.1	109	2 C83344	hypothetical prote
11	7	3.1	110	2 S40503	beta-1-adrenergic
12	7	3.1	119	2 A83896	hypothetical prote
13	7	3.1	122	2 T52448	flowering locus T
14	7	3.1	134	2 PC4214	phosphatidylethano
15	7	3.1	140	2 A38845	flagellar protein
16	7	3.1	152	2 D97462	hypothetical prote
17	7	3.1	152	2 AF2680	transcription regu
18	7	3.1	152	2 PC4216	phosphatidylethano
19	7	3.1	152	2 A44947	16k antigen precu
20	7	3.1	175	2 T52446	FT protein homolog
21	7	3.1	175	2 T52447	FT protein [valida
22	7	3.1	186	2 S00056	basic cytosolic pr
23	7	3.1	186	2 S18358	23K protein - rat
24	7	3.1	187	2 S46485	phosphatidylethano
25	7	3.1	187	2 I53745	phosphatidylethano
26	7	3.1	187	2 A36126	23K phosphatidyle
27	7	3.1	190	2 T08258	conserved hypothet
28	7	3.1	194	2 S77566	hypothetical prote
29	7	3.1	195	2 C73490	hypothetical prote

hypothetical prote
TF51 related prote
hypothetical prote
hypothetical prote
two-component resp
hypothetical prote
integral membrane
probable ABC-trans
hypothetical prote
probable lipoprote
lic-1 protein B -
hypothetical prote
conserved hypothet
wnt-6 protein - mo
soluble-type glyco
ubiquinol-cytochro
ornithine carbamoy
hypothetical prote
hypothetical prote
macrolide 3-O-acyl
probable MFS trans
membrane protein,
probable membrane
tetrahydrofolylpol
conserved hypothet
probable oxidoredu
fumarate hydratase
fumarate hydratase
hypothetical prote
probable phospho-s
hypothetical prote
amino acid transpo
hypothetical prote
amino acid ABC tra
UDP-N-acetylmurano
meso-diaminopimela
meso-diaminopimela
hypothetical prote
probable integral
probable MFS trans
laccase (EC 1.10.3
Na+/H+ antiporter
hypothetical prote
membrane transloca
probable sodium/hy
h+-transporting AT
probable DNA-direc
probable thyroid r
probable two-compo
hypothetical prote
zinc finger RNA bi
zinc metalloprotei
hypothetical prote
glyceraldehyde-3-p
benzphetamine N-de
ribosomal protein
hypothetical prote
hypothetical prote
conserved domain p
hypothetical prote
hypothetical prote
NADH2 dehydrogenas
trab protein - Agr
probable molybdopt
molybdopterin conv
oxaloacetate decar
conjugated transfer
hypothetical prote
sodium ion pump ox
gonadoliberin II p
hypothetical prote
hypothetical prote
conserved hypothet

687	6	2.7	605	2	C90613	NADH dehydrogenase	760	6	2.7	684	2	A53019	collagen alpha 1(X
688	6	2.7	605	2	T11529	NADH2 dehydrogenas	761	6	2.7	684	2	T36771	probable integral
689	6	2.7	605	2	C90623	NADH2 dehydrogenas	762	6	2.7	684	2	T32024	hypothetical prote
690	6	2.7	605	2	T11085	NADH2 dehydrogenas	763	6	2.7	685	1	A47102	system b(0,+)-amin
691	6	2.7	606	1	QXBO5M	NADH2 dehydrogenas	764	6	2.7	685	2	JC6331	rho-type guanine e
692	6	2.7	606	2	T11503	NADH2 dehydrogenas	765	6	2.7	687	2	B81027	glycyl-tRNA synthe
693	6	2.7	606	2	T11150	NADH2 dehydrogenas	766	6	2.7	687	2	G81970	probable glycine-t
694	6	2.7	606	2	T11334	NADH2 dehydrogenas	767	6	2.7	687	2	T02459	probable beta-amyl
695	6	2.7	606	2	CS8851	NADH2 dehydrogenas	768	6	2.7	691	2	D96805	probable acyl-CoA
696	6	2.7	606	2	S41830	NADH2 dehydrogenas	769	6	2.7	694	2	S73403	fructose-permease
697	6	2.7	606	2	T45560	NADH2 dehydrogenas	770	6	2.7	700	2	A84243	phosphoribosylform
698	6	2.7	606	2	T10982	NADH2 dehydrogenas	771	6	2.7	702	2	D83205	probable oxidoredu
699	6	2.7	606	2	T11060	NADH2 dehydrogenas	772	6	2.7	703	2	H86349	protein F8K7.9 lim
700	6	2.7	606	2	C90627	NADH dehydrogenase	773	6	2.7	704	2	AE2107	serine/threonine k
701	6	2.7	606	2	C75431	GTP-binding transl	774	6	2.7	706	1	WZBED8	gene 45 protein -
702	6	2.7	607	1	QXWS5M	NADH2 dehydrogenas	775	6	2.7	706	2	T42589	gene 45 protein -
703	6	2.7	607	2	T11032	NADH2 dehydrogenas	776	6	2.7	709	2	E82298	polyribonucleotide
704	6	2.7	607	2	S36006	NADH2 dehydrogenas	777	6	2.7	709	2	S38883	polyribonucleotide
705	6	2.7	609	2	S04757	NADH2 dehydrogenas	778	6	2.7	710	2	S04128	phenylalanine ammo
706	6	2.7	609	2	T11310	NADH2 dehydrogenas	779	6	2.7	715	2	A97449	methyl-accepting c
707	6	2.7	609	2	T11774	NADH2 dehydrogenas	780	6	2.7	720	2	E84456	probable acyl-CoA
708	6	2.7	610	2	T11544	NADH2 dehydrogenas	781	6	2.7	721	2	F82198	probable toxin sec
709	6	2.7	611	2	CS9893	NADH2 dehydrogenas	782	6	2.7	725	2	S38087	hypothetical prote
710	6	2.7	611	2	T11297	NADH2 dehydrogenas	783	6	2.7	725	2	S13426	multidrug resistan
711	6	2.7	611	2	S68138	NADH2 dehydrogenas	784	6	2.7	726	1	UYFVS1	noncapsid protein
712	6	2.7	611	2	S19434	probable transport	785	6	2.7	726	2	T34638	hypothetical prote
713	6	2.7	612	2	S35471	NADH2 dehydrogenas	786	6	2.7	729	2	A49120	fibroblast growth
714	6	2.7	612	2	T14101	NADH2 dehydrogenas	787	6	2.7	734	2	B70173	methionine-tRNA li
715	6	2.7	612	2	T14104	NADH2 dehydrogenas	788	6	2.7	737	1	S14408	translation elonga
716	6	2.7	612	2	T09867	NADH2 dehydrogenas	789	6	2.7	742	2	T35650	probable ATP-depen
717	6	2.7	612	2	T09957	NADH2 dehydrogenas	790	6	2.7	747	2	D75436	ATP-dependent Clp
718	6	2.7	612	2	T11830	NADH2 dehydrogenas	791	6	2.7	747	2	T40728	hypothetical prote
719	6	2.7	613	2	T11464	NADH2 dehydrogenas	792	6	2.7	753	2	T46614	chemotaxis protein
720	6	2.7	613	2	T00448	hypothetical prote	793	6	2.7	754	2	S41391	gelsolin - America
721	6	2.7	613	2	I33295	X-linked PEST-cont	794	6	2.7	754	2	S53373	gelsolin - America
722	6	2.7	615	2	G83419	probable binding p	795	6	2.7	756	2	H75016	hypothetical prote
723	6	2.7	616	2	S33908	glucan 1,4-alpha-g	796	6	2.7	759	2	E84854	probable copper am
724	6	2.7	616	2	H84474	probable Athila re	797	6	2.7	760	2	T01441	hypothetical prote
725	6	2.7	616	2	A12851	hypothetical prote	798	6	2.7	769	2	F81415	DNA topoisomerase
726	6	2.7	617	1	RNJV7A	transcription init	799	6	2.7	778	2	H96649	protein F2401.4 [i
727	6	2.7	617	2	AF1284	5-methyltetrahydro	800	6	2.7	784	2	E72515	probable DNA-direc
728	6	2.7	617	2	A11655	5-methyltetrahydro	801	6	2.7	784	2	T74270	hypothetical prote
729	6	2.7	618	2	T05518	hypothetical prote	802	6	2.7	793	2	T34270	pyruvate, water di
730	6	2.7	619	2	F82984	hypothetical prote	803	6	2.7	796	1	JV0107	glucose dehydrogen
731	6	2.7	621	1	S20145	replication factor	804	6	2.7	796	2	H85495	glucose dehydrogen
732	6	2.7	623	2	G64571	conserved hypotet	805	6	2.7	797	2	D86269	hypothetical prote
733	6	2.7	623	2	C71865	hypothetical prote	806	6	2.7	797	2	T33673	hypothetical prote
734	6	2.7	624	2	S64118	probable membrane	807	6	2.7	802	2	A83125	probable TonB-depe
735	6	2.7	627	2	S48968	NDR80 protein - ye	808	6	2.7	808	1	QPKEX	glucose dehydrogen
736	6	2.7	630	2	H89056	protein K09H11.4 [809	6	2.7	809	2	B87260	sensory box/GDEF
737	6	2.7	631	2	H96763	feebly-like protei	810	6	2.7	812	2	H87386	hypothetical prote
738	6	2.7	632	2	S68599	phosphotransferase	811	6	2.7	812	2	AC3304	non-motile and pha
739	6	2.7	633	2	G97628	ATP-binding protei	812	6	2.7	813	2	AC3304	type I restriction
740	6	2.7	636	2	T35182	probable ABC-type	813	6	2.7	815	2	C71810	3-hydroxyacyl-CoA
741	6	2.7	640	2	S62747	homeotic protein A	814	6	2.7	815	2	E70021	endopeptidase [imp
742	6	2.7	641	2	PH1919	FL-160-4 protein -	815	6	2.7	818	2	F98919	leucyl-tRNA synthe
743	6	2.7	643	2	S70592	NADH2 dehydrogenas	816	6	2.7	819	2	G81698	leucine-tRNA ligas
744	6	2.7	643	2	T28867	hypothetical prote	817	6	2.7	819	2	C71544	leucyl tRNA synthe
745	6	2.7	647	2	AE1054	2',3'-cyclic-nucle	818	6	2.7	820	2	A86510	leucine-tRNA ligas
746	6	2.7	649	2	AH0493	methyl-accepting c	819	6	2.7	820	2	C72113	hypothetical prote
747	6	2.7	656	2	B82056	glutathione-regula	820	6	2.7	823	2	A96501	probable integral
748	6	2.7	656	2	D96831	hypothetical prote	821	6	2.7	823	2	T35280	endothelin convert
749	6	2.7	662	2	F90442	hypothetical prote	822	6	2.7	825	2	I46078	DNA-binding protei
750	6	2.7	671	2	T02504	hypothetical prote	823	6	2.7	827	2	S50714	hypothetical prote
751	6	2.7	672	2	A56765	sodium-glucose cot	824	6	2.7	836	2	T42323	DNA topoisomerase
752	6	2.7	672	2	A42251	nucleoside transpo	825	6	2.7	839	2	S32158	DNA topoisomerase
753	6	2.7	672	2	F71424	hypothetical prote	826	6	2.7	840	2	C83378	probable ATP-depen
754	6	2.7	673	2	AD2667	chemotaxis methyl-	827	6	2.7	842	2	C81395	alanine-tRNA ligas
755	6	2.7	676	2	A40363	DNA ligase (NAD) (828	6	2.7	845	2	S83193	translation elonga
756	6	2.7	676	2	T34029	hypothetical prote	829	6	2.7	855	2	B31933	DNA mismatch repai
757	6	2.7	676	2	S67136	hypothetical prote	830	6	2.7	855	2	A53296	DNA mismatch repai
758	6	2.7	678	1	B75360	2',3'-cyclic-nucle	831	6	2.7	860	2	JCS986	A-kinase anchoring
759	6	2.7	683	1	A41785	system b(0,+) amin	832	6	2.7	863	1	S51789	VLDL receptor prec

833	6	2.7	863	2	G96964	probable permease, DNA topoisomerase	906	6	2.7	1317	2	T14595	polyprotein - maiz
834	6	2.7	865	2	H81749	alanine-tRNA ligase	907	6	2.7	1334	2	T19493	hypothetical prote
835	6	2.7	877	2	H71647	probable RNA ligase	908	6	2.7	1345	2	T41960	major capsid prote
836	6	2.7	880	2	T02245	hypothetical prote	909	6	2.7	1366	2	T35985	probable large pro
837	6	2.7	883	2	A84210	hypothetical prote	910	6	2.7	1370	1	VCBECA	major capsid prote
838	6	2.7	883	2	C83385	hypothetical prote	911	6	2.7	1370	2	T03120	major capsid prote
839	6	2.7	888	2	H71280	probable antidioti	912	6	2.7	1371	1	VCBEW7	major capsid prote
840	6	2.7	891	2	B82495	probable NADH dehy	913	6	2.7	1381	2	S55619	capsid protein 25
841	6	2.7	892	2	T50985	related to transcr	914	6	2.7	1382	1	INHRUR	insulin receptor p
842	6	2.7	894	2	F84870	hypothetical prote	915	6	2.7	1396	1	VCBE40	major capsid prote
843	6	2.7	905	2	G84582	hypothetical prote	916	6	2.7	1396	2	A44453	translation initia
844	6	2.7	905	2	A28892	hypothetical prote	917	6	2.7	1402	2	I46707	translation initia
845	6	2.7	905	2	C97668	ABC transporter re	918	6	2.7	1420	2	T37781	probable cytoskele
846	6	2.7	910	2	C69069	cation-transportin	919	6	2.7	1442	2	S72441	protein-tyrosine-p
847	6	2.7	916	2	T03323	gene l16 protein -	920	6	2.7	1446	1	A45344	immediate-early pr
848	6	2.7	920	2	T41050	conserved hypothet	921	6	2.7	1460	1	EDBEIF	immediate-early pr
849	6	2.7	929	2	H84582	hypothetical prote	922	6	2.7	1460	2	D81675	polymorphic membra
850	6	2.7	943	2	JE0121	hypothetical 107.4	923	6	2.7	1468	2	S58250	DNA-directed DNA p
851	6	2.7	944	2	H64650	translation initia	924	6	2.7	1471	2	T40117	myosin-2 isoform -
852	6	2.7	949	2	E71940	translation initia	925	6	2.7	1473	2	T38791	probable ferredoxi
853	6	2.7	950	2	E70203	exonuclease SbcC (926	6	2.7	1501	2	T29094	ribulose-bisphosph
854	6	2.7	966	2	T50668	villin 3 (imported	927	6	2.7	1503	2	T43166	alpha-2-macroglobu
855	6	2.7	984	1	A34076	protein-tyrosine k	928	6	2.7	1532	2	A26039	IgA-specific metal
856	6	2.7	986	2	A87590	hypothetical prote	929	6	2.7	1547	2	A12043	hypothetical prote
857	6	2.7	992	1	GNWVR3	structural polypro	930	6	2.7	1592	2	S48933	probable transport
858	6	2.7	995	2	C83203	probable serine pr	931	6	2.7	1655	2	T32633	hypothetical prote
859	6	2.7	996	2	S70646	transcription fact	932	6	2.7	1668	2	A60272	IgA-specific metal
860	6	2.7	1002	2	S70292	FUN12 protein - ye	933	6	2.7	1684	2	JW0057	gravin - human
861	6	2.7	1004	2	A48821	Wnt-5 protein - fr	934	6	2.7	1690	2	T40847	probable rRNA biog
862	6	2.7	1008	2	T30544	major surface glyc	935	6	2.7	1773	2	T05128	hypothetical prote
863	6	2.7	1012	2	S68259	DNA polymerase gam	936	6	2.7	1787	2	AC2009	serine/threonine k
864	6	2.7	1013	2	JQ1920	DNA-directed DNA p	937	6	2.7	1800	2	A11918	serine/threonine k
865	6	2.7	1014	2	T30431	DNA-directed DNA p	938	6	2.7	1804	2	AF2250	serine/threonine k
866	6	2.7	1015	1	G70389	formate dehydrogen	939	6	2.7	1825	2	S13507	microtubule-associ
867	6	2.7	1021	2	I39207	leukocyte surface	940	6	2.7	1830	2	A37981	microtubule-associ
868	6	2.7	1023	1	A24639	Na+/K+-exchanging	941	6	2.7	1882	2	T00089	hypothetical prote
869	6	2.7	1027	2	F87370	alpha-L-rhamnosida	942	6	2.7	1884	1	A45353	genome polyprotein
870	6	2.7	1045	2	S23570	pol polyprotein ho	943	6	2.7	1885	2	JQ2183	hypothetical 216.5
871	6	2.7	1048	2	S27763	Ca2+-transporting	944	6	2.7	1963	2	B98002	IgA-specific metal
872	6	2.7	1048	2	T04172	Ca2+-transporting	945	6	2.7	2004	2	F95133	immunoglobulin A1
873	6	2.7	1051	2	A35761	cell surface glyco	946	6	2.7	2014	2	S46622	probable membrane
874	6	2.7	1051	2	A40021	integrin alpha-3 c	947	6	2.7	2073	2	T39207	fatty acid synthas
875	6	2.7	1053	2	I55534	VLA-3 alpha subuni	948	6	2.7	2073	2	T43311	fatty acyl-CoA syn
876	6	2.7	1054	2	T01556	Ca2+-transporting	949	6	2.7	2108	2	H70819	probable polyketid
877	6	2.7	1056	2	T02930	lysine-ketoglutar	950	6	2.7	2109	2	I38414	transcription fact
878	6	2.7	1063	1	GNWV77	structural polypro	951	6	2.7	2128	2	I52577	beta-spectrin - mo
879	6	2.7	1063	1	GNWVR4	structural polypro	952	6	2.7	2143	2	G96595	hypothetical prote
880	6	2.7	1063	1	GNWVR4	structural polypro	953	6	2.7	2205	1	MMWVRN	nonstructural poly
881	6	2.7	1063	2	T03743	bifocal protein -	954	6	2.7	2298	2	T49648	hypothetical prote
882	6	2.7	1065	1	RNLVB	DNA-directed RNA p	955	6	2.7	2352	2	C83229	probable non-ribos
883	6	2.7	1068	2	E81965	probable outer mem	956	6	2.7	2464	1	QRMSP1	microtubule-associ
884	6	2.7	1082	2	H81020	serotype-1-specifi	957	6	2.7	2684	2	A96521	protein F21D18.22
885	6	2.7	1099	2	I46497	bumetanide-sensiti	958	6	2.7	2685	2	T38755	hypothetical prote
886	6	2.7	1099	2	I46498	bumetanide-sensiti	959	6	2.7	2693	2	A40743	IP3 receptor, XIP3
887	6	2.7	1099	2	I46496	bumetanide-sensiti	960	6	2.7	2706	2	T28155	variant-specific s
888	6	2.7	1099	2	T30307	rexB protein - lac	961	6	2.7	2723	2	T03221	probable polyketid
889	6	2.7	1120	2	F90693	mechanosensitive c	962	6	2.7	2970	2	T08839	polyprotein - maxm
890	6	2.7	1120	2	B85544	probable membrane	963	6	2.7	3005	2	T08841	polyprotein - dour
891	6	2.7	1120	2	H64776	hypothetical prote	964	6	2.7	3263	2	B82410	hypothetical prote
892	6	2.7	1122	2	T47424	probable two-compo	965	6	2.7	3335	2	H81702	adherence factor T
893	6	2.7	1126	2	A96032	hypothetical prote	966	6	2.7	3388	1	GNWVDP	genome polyprotein
894	6	2.7	1160	2	T23713	hypothetical prote	967	6	2.7	3390	1	GNWVJ3	genome polyprotein
895	6	2.7	1205	2	A55015	bumetanide-sensiti	968	6	2.7	3391	1	GNWVJA	genome polyprotein
896	6	2.7	1207	2	T00378	KIAA0641 protein -	969	6	2.7	3421	1	WZBEB6	367K tegument prot
897	6	2.7	1212	2	A57187	bumetanide-sensiti	970	6	2.7	3433	1	S28381	utrophin - human
898	6	2.7	1221	2	E83327	conserved hypothet	971	6	2.7	3488	2	T34418	hypothetical prote
899	6	2.7	1224	2	E71611	hypothetical prote	972	6	2.7	3534	2	T42567	tegument protein 2
900	6	2.7	1246	2	S56752	helicase SKI2W - h	973	6	2.7	3864	2	D87757	protein C44B4.1a [
901	6	2.7	1274	2	T25024	hypothetical prote	974	6	2.7	4574	2	G02520	plectin - human
902	6	2.7	1286	2	T23714	hypothetical prote	975	6	2.7	4684	2	A59404	plectin [imported]
903	6	2.7	1290	2	AE3192	two-component hybr	976	6	2.7	5032	1	A35041	ryanodine receptor
904	6	2.7	1298	2	B83175	phosphoribosylform	977	6	2.7	5035	1	I46646	ryanodine receptor
905	6	2.7	1314	2	A85176	hypothetical prote	978	6	2.7	5037	2	B35041	ryanodine receptor

A;Residues: 1-24 <SIN>
A;Cross-references: UNIPROT:Q9PS43; UNIPROT:Q9PRV4
A;Note: sequence extracted from NCB1 backbone (NCBIP:113919)
C;Superfamily: cytochrome P450 homology
C;Keywords: electron transfer; endoplasmic reticulum; heme; membrane protein; monooxygenase

Query Match 3.1%; Score 7; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VTAAALLL 14
|||||
DB 3 VTAAALLL 9

RESULT 6

A61056
aminopyrine N-demethylase (EC 1.14.14.-) cytochrome P450 PB-A - chicken. (fragment)
N;Alternate names: 7-ethoxycoumarin O-deethylase; phenobarbital-induced 52 kDa cytochrome
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: C44107; A61056; S13263
R;Nakai, K.; Ward, A.M.; Gannon, M.; Rifkind, A.B.

J. Biol. Chem. 267, 19503-19512, 1992
A;Title: Beta-naphthoflavone induction of a cytochrome P-450 arachidonic acid epoxigenase
A;Reference number: A44107; MUID:92406903; PMID:1527070

A;Accession: C44107

A;Molecule type: protein

A;Residues: 1-26 <NAK>

A;Cross-references: UNIPROT:Q9PS43

A;Experimental source: embryo liver

A;Note: sequence extracted from NCB1 backbone (NCBIP:113920)

R;Gupta, R.P.; Lapadula, D.M.; Abou-Donia, M.B.

Comp. Biochem. Physiol. C 96, 163-176, 1990

A;Title: Purification and characterization of cytochrome P-450 isozymes from phenobarbital
A;Reference number: A61056; MUID:91130218; PMID:1980873

A;Accession: A61056

A;Molecule type: protein

A;Residues: 1-19 <GUP>

R;Gupta, R.P.; Lapadula, D.M.; Abou-Donia, M.B.

Arch. Biochem. Biophys. 282, 170-182, 1990

A;Title: Purification and characterization of cytochrome P450 isozymes from beta-naphthol
A;Accession: S13263

A;Reference number: S13263; MUID:91024193; PMID:2171427

A;Molecule type: protein

A;Residues: 1-24 <GUP>

C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C;Keywords: electron transfer; endoplasmic reticulum; heme; membrane protein; monooxygenase

Query Match 3.1%; Score 7; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VTAAALLL 14
|||||
DB 3 VTAAALLL 9

RESULT 7

B4107
cytochrome P450 NF3, beta-naphthoflavone-induced (N-terminal) - chicken (fragment)
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Gallus gallus (chicken)
C;Date: 27-Apr-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C;Accession: B4107

R;Nakai, K.; Ward, A.M.; Gannon, M.; Rifkind, A.B.

J. Biol. Chem. 267, 19503-19512, 1992

A;Title: Beta-naphthoflavone induction of a cytochrome P-450 arachidonic acid epoxigenase
A;Reference number: A44107; MUID:92406903; PMID:1527070

A;Accession: B4107

A;Molecule type: protein

A;Residues: 1-26 <NAK>

A;Cross-references: UNIPROT:Q9PS44

A;Experimental source: embryo liver

A;Note: sequence extracted from NCB1 backbone (NCBIP:113919)

C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase

Query Match 3.1%; Score 7; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VTAAALLL 14
|||||
DB 3 VTAAALLL 9

RESULT 8

S29135
aminopyrine N-demethylase (EC 1.14.14.-) cytochrome P450 betaNF-A1 - chicken (fragment)
N;Alternate names: 7-ethoxycoumarin O-deethylase
C;Species: Gallus gallus (chicken)

C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 16-Aug-2004

C;Accession: S29135

R;Gupta, R.P.; Lapadula, D.M.; Abou-Donia, M.B.

Arch. Biochem. Biophys. 282, 170-182, 1990

A;Title: Purification and characterization of cytochrome P450 isozymes from beta-naphthol

A;Reference number: S13263; MUID:91024193; PMID:2171427

A;Accession: S29135

A;Molecule type: protein

A;Residues: 1-28 <GUP>

C;Superfamily: cytochrome P450 homology

C;Keywords: electron transfer; endoplasmic reticulum; heme; membrane protein; monooxygenase

Query Match 3.1%; Score 7; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VTAAALLL 14
|||||
DB 3 VTAAALLL 9

RESULT 9

S29136
aminopyrine N-demethylase (EC 1.14.14.-) cytochrome P450 betaNF-A2 - chicken (fragment)
N;Alternate names: 7-ethoxycoumarin O-deethylase
C;Species: Gallus gallus (chicken)

C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 16-Aug-2004

C;Accession: S29136

R;Gupta, R.P.; Lapadula, D.M.; Abou-Donia, M.B.

Arch. Biochem. Biophys. 282, 170-182, 1990

A;Title: Purification and characterization of cytochrome P450 isozymes from beta-naphthol

A;Reference number: S13263; MUID:91024193; PMID:2171427

A;Accession: S29136

A;Molecule type: protein

A;Residues: 1-28 <GUP>

A;Cross-references: UNIPROT:Q7LZ56

C;Superfamily: cytochrome P450 homology

C;Keywords: electron transfer; endoplasmic reticulum; heme; membrane protein; monooxygenase

Query Match 3.1%; Score 7; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VTAAALLL 14
|||||
DB 3 VTAAALLL 9

RESULT 10

C83344

hypothetical protein PA2405 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: C83344
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Boudry, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83344
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <STO>
A;Cross-references: UNIPROT:Q91176; GB:AE004668; GB:AE004091; NID:G9948446; PIDN:AAG0579
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2405

Query Match 3.1%; Score 7; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AALLGL 16
Db 13 AALLGL 19

RESULT 11
S40503
beta-1-adrenergic receptor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Oct-1994 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S40503
R;Castella, L.; Muzin, P.; Revelli, J.P.; Ricquier, D.; Giacobino, J.P.
Biochem. J. 297, 93-97, 1994
A;Title: Expression of beta(1)- and beta(3)-adrenergic-receptor messages and adenylylate
ite fat.
A;Reference number: S40503; MUID:94107292; PMID:7904157
A;Accession: S40503
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-110 <CAS>
A;Cross-references: UNIPROT:Q9TS16
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 3.1%; Score 7; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 PDAPSRA 103
Db 96 PDAPSRA 102

RESULT 12
A83896
hypothetical protein BH1969 [imported] - *Bacillus halodurans* (strain C-125)
C;Species: *Bacillus halodurans*
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A83896
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83896
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <STO>
A;Cross-references: UNIPROT:Q9KBF9; GB:AP001513; GB:BA000004; NID:G10174345; PIDN:BA056
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1969

Query Match 3.1%; Score 7; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VTAALL 14
Db 8 VTAALL 14

RESULT 13
T52448
flowering locus T protein, splice variant 2 [validated] - *Arabidopsis thaliana*
N;Alternate names: FT protein
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52448
R;Kobayashi, Y.; Kaya, H.; Goto, K.; Iwabuchi, M.; Araki, T.
Science 286, 1960-2, 1999
A;Title: A pair of related genes with antagonistic roles in mediating flowering signals
A;Reference number: Z25350; MUID:20050959; PMID:10583960
A;Accession: T52448
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-122 <KOB>
A;Cross-references: UNIPROT:Q9SXZ2; EMBL:AB027505; PIDN:BAA77839.1
A;Experimental source: cultivar Landsberg erecta
C;Genetics:
A;Gene: FT
C;Function:
A;Description: promotes flowering [validated, MUID:20050958]
A;Note: is positively regulated by transcription factor CONSTANS

Query Match 3.1%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 LVMVDP 98
Db 67 LVMVDP 73

RESULT 14
PC4214
phosphatidylethanolamine binding protein Ovd3 - nematode (*Onchocerca volvulus*) (fragment)
C;Species: *Onchocerca volvulus*
C;Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: PC4214
R;Ertmann, K.D.; Gallin, M.Y.
Gene 174, 203-207, 1996
A;Title: *Onchocerca volvulus*: Identification of cDNAs encoding a putative phosphatidyl-e
A;Reference number: PC4214; MUID:97045913; PMID:8890735
A;Accession: PC4214
A;Molecule type: mRNA
A;Residues: 1-134 <ERT>
A;Cross-references: UNIPROT:P54188; EMBL:X87989; NID:G1143530; PID:G1143531
C;Genetics:
A;Introns: 34/3; 52/2; 81/1; 129/3
C;Superfamily: *Caenorhabditis elegans* hypothetical protein Y69E1A.5

Query Match 3.1%; Score 7; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 DPAPSR 102
Db 35 DPAPSR 41

RESULT 15
A38845
flagellar protein required for flagellar formation flilL - *Bacillus subtilis*
N;Alternate names: Flil protein homolog
C;Species: *Bacillus subtilis*
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004

C:Accession: A38845; A39136; H69624; S14503
 R:Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
 J. Bacteriol. 173, 3573-3579, 1991
 A:Title: The flhA locus of *Bacillus subtilis* is part of a large operon coding for flagel
 A:Reference number: A42365; MUID:91258343; PMID:1828465
 A:Accession: A38845
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-140 <ALB>
 A:Cross-references: UNIPROT:P23452; EMBL:X56049; NID:G39904; PIDN:CAA39529.1; PID:G39913
 R:Zuberi, A.R.; Bischoff, D.S.; Ordal, G.W.
 J. Bacteriol. 173, 710-719, 1991
 A:Title: Nucleotide sequence and characterization of a *Bacillus subtilis* gene encoding a
 A:Reference number: A39136; MUID:91100360; PMID:1898932
 A:Accession: A39136
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 57-140 <ZUB>
 A:Cross-references: GB:M37691; NID:G142920; PIDN:AAA22445.1; PID:G142921
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.;
 Nature 390, 249-256, 1997
 A:Authors: Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
 wood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.;
 Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber,
 A:Authors: Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigu
 , K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, D.; Porwol
 , Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.; Schleic
 A:Authors: Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serro
 ; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa,
 A:Authors: Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: H69624
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-140 <KUN>
 A:Cross-references: GB:Z99112; GB:AL009126; NID:G2633902; PIDN:CAB13503.1; PID:G2634002
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: flhL
 C:Superfamily: flagellar formation protein flhL
 C:Keywords: flagellar rotation

Query Match 3.1%; Score 7; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 YLQEGKV 161
 |||||
 Db 123 YLQEGKV 129

Search completed: January 31, 2005, 15:12:28
 Job time :. 48 secs

